

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 24, 2004, 06:09:02 ; Search time 6028 Seconds
(without alignments)
10590.759 Million cell updates/sec

Title: US-10-089-364-3
Perfect score: 1350
Sequence: 1 atgttgccagtcctccgcctc.....ggggcgagtggtttgcttag 1350

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*
1: gb.ba.*
2: gb.hg.*
3: gb.in.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.sy.*
13: gb.un.*
14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1347	99.8	1404	6 A19452	A19452 phytase cDN
2	1347	99.8	1404	6 I13430	I13430 Sequence 33
3	1347	99.8	1404	6 I33881	I33881 Sequence 19
4	1347	99.8	1404	6 AR195149	AR195149 Sequence
5	1347	99.8	2000	8 ANPHYAG	Z16414 Aspergillus
6	1347	99.8	2665	8 ANPHYATSE	M94550 Aspergillus
7	1347	99.8	6756	6 A19451	A19451 phytase gen
8	1347	99.8	6756	6 I13429	I13429 Sequence 31
9	1347	99.8	6756	6 AR195148	AR195148 Sequence
10	1275	94.4	2363	6 AR018076	AR018076 Sequence
11	1275	94.4	2363	6 AR051916	AR051916 Sequence
12	1275	94.4	2379	6 AR053934	AR053934 Sequence
13	1275	94.4	2379	8 ANPHYATAS	L0421 Aspergillus
14	1270.2	94.1	1525	8 AY426977	AY426977 Aspergill
15	1268.6	94.0	1528	8 AR218813	AR218813 Aspergill
16	1204.6	89.2	1506	8 AY513749	AY513749 Aspergill
17	1188.6	88.0	1347	8 AF537344	AF537344 Aspergill
18	1185.4	87.8	1590	8 AY013315	AY013315 Aspergill
19	1183.8	87.7	1347	8 AY603416	AY603416 Aspergill

20	1183.8	87.7	1347	8 AY615712	AY615712 Aspergill
21	1182.2	87.6	1515	6 AR116878	AR116878 Sequence
22	1182.2	87.6	1515	6 AR175871	AR175871 Sequence
23	1182.2	87.6	1515	6 AR306351	AR306351 Sequence
24	1182.2	87.6	1515	6 AB022700	AB022700 Aspergill
25	1182	87.6	1350	12 AF353576	AF353576 Synthetic
26	1167.2	86.5	1332	6 AR116877	AR116877 Sequence
27	1167.2	86.5	1332	6 AR175870	AR175870 Sequence
28	1167.2	86.5	1332	6 AR306350	AR306350 Sequence
29	1152.6	85.4	1335	6 AX960554	AX960554 Sequence
30	1119	82.9	1335	6 AX960552	AX960552 Sequence
31	1111	82.3	1335	6 AX960550	AX960550 Sequence
32	1104.2	81.8	1350	12 AR295325	AR295325 Synthetic
33	1075	79.6	1404	12 AX150806	AX150806 Synthetic
34	841	62.3	1347	12 AF542235	AF542235 Synthetic
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36	810.4	60.0	1912	6 AR170094	AR170094 Sequence
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ALIGNMENTS

RESULT 1
A19452 LOCUS A19452 1404 bp RNA linear PAT 10-JUN-1994
DEFINITION Phytase cDNA fragment.
ACCESSION A19452
VERSION A19452.1 GI:583195
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 1404)
AUTHORS Veenstra, A.E., Luiten, R.G.M. and Selten, G.C.M.
TITLE Cloning and expression of microbial phytase
JOURNAL Patent: EP 0420358-A 41 03-APR-1991;
FEATURES
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Location/Qualifiers
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KLSPCDLFTHDENLYDLQSLKKYGHGACNPLGTCQGVGNELARLTHSPVHD
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Query Match 99.8%; Score 1347; DB 6; Length 1404;
Best Local Similarity 100.0%; Pred. No. 2.9e-291;

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424 TCCTCTGGCTCCAGCGCGGTGATCGCTCGGCAAGAAATTCATCGAGGCTTCAGAGC 483
478 TCCTCTGGCTCCAGCGCGGTGATCGCTCGGCAAGAAATTCATCGAGGCTTCAGAGC 537
484 ACCAAGCTGAAGGATCTCGTCCGACCGCGCAATCGTCGCCCAAGATCGAGCTGGTC 543
538 ACCAAGCTGAAGGATCTCGTCCGACCGCGCAATCGTCGCCCAAGATCGAGCTGGTC 597
544 ATTTCCAGGCGAGCTCATTCACACAACTCTCGACCCAGGCACTGCTCTCGAA 603
598 ATTTCCAGGCGAGCTCATTCACACAACTCTCGACCCAGGCACTGCTCTCGAA 657
604 GACAGCAATTTGGCGGATACCGTTCGAAGCAATTTACCGCCACGTTTCCTCCCTCAAT 663
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664 CGTCAAGCTGAGAGACGACTCTCGCGGTGATCTCTACACACAGAAAGTGAAGTAC 723
718 CGTCAAGCTGAGAGACGACTCTCGCGGTGATCTCTACACACAGAAAGTGAAGTAC 777
724 CTCAATGACATGTCTCTCTCGACCACTCTCCACAGCACCGTTCGACACCAAGCTGTCC 783
778 CTCAATGACATGTCTCTCTCGACCACTCTCCACAGCACCGTTCGACACCAAGCTGTCC 837
784 CCCTTCTGTGACCTGTTCACCCATGACGAATGGAATCAACTACGATACCTCCAGTCTTG 843
838 CCCTTCTGTGACCTGTTCACCCATGACGAATGGAATCAACTACGATACCTCCAGTCTTG 897
844 AAAAGTATTACGGCCATGTCAGGTAACCGCTCGGCGCGACCCAGGCGGTGCGTAC 903
898 AAAAGTATTACGGCCATGTCAGGTAACCGCTCGGCGCGACCCAGGCGGTGCGTAC 957
904 GCTAACAGCTCATTCGCGCGGTCTGACCACTCGGCTCTCCACGATGACACCAAGTTCAC 963
958 GCTAACAGCTCATTCGCGCGGTCTGACCACTCGGCTCTCCACGATGACACCAAGTTCAC 1017
964 CACATTTGGACTCGAGCGGCTACCTTTCCGCTCAACTCTACTCTCTACGCGGACTTT 1023
1018 CACATTTGGACTCGAGCGGCTACCTTTCCGCTCAACTCTACTCTCTACGCGGACTTT 1077
1024 TCAGATGACAAAGGATCATCTCCATCTCTTTCTTTTGTGATGATGATGATGATGATGAT 1083
1078 TCAGATGACAAAGGATCATCTCCATCTCTTTCTTTTGTGATGATGATGATGATGATGAT 1137
1084 CCGCTATCTACCAAGCGGTGAGAAATATCACCAAGAGATGATGATGATGATGATGATGAT 1143
1138 CCGCTATCTACCAAGCGGTGAGAAATATCACCAAGAGATGATGATGATGATGATGATGAT 1197
1144 ACGGTCGGTTTGGCTTCGCTTCTAGCTGAGATGATGATGATGATGATGATGATGATGAT 1203
1198 ACGGTCGGTTTGGCTTCGCTTCTAGCTGAGATGATGATGATGATGATGATGATGATGAT 1257
1204 CCGTGTGTCTGTCTGTTTAAATGATGCGGTTCTCCGCTGATGATGATGATGATGATGAT 1263
1258 CCGTGTGTCTGTCTGTTTAAATGATGCGGTTCTCCGCTGATGATGATGATGATGATGAT 1317
1264 GCTTTGGGAGATGATACCGGATGATGATGATGATGATGATGATGATGATGATGATGAT 1323
1318 GCTTTGGGAGATGATACCGGATGATGATGATGATGATGATGATGATGATGATGATGAT 1377
1324 GGTGATTCGGCGGAGTGTGTTTGTCTAG 1350
1378 GGTGATTCGGCGGAGTGTGTTTGTCTAG 1404

RESULT 3
LOCUS I33881 1404 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 19 from patent US 5593963.
ACCESSION I33881
VERSION I33881.1 GI:1824672

KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1404)
AUTHORS Van Ooijen,A.J., Rietveld,K., Hoekema,A., Pen,J., Sijmons,P.C.
and Verwoerd,T.C.
TITLE Expression of phytoase in plants
JOURNAL Patent: US 5593963-A 19 14-JAN-1997;
FEATURES
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/organism="unknown"
/mol_type="unassigned DNA"
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Query Match 99.8%; Score 1347; DB 6; Length 1404;
Best Local Similarity 100.0%; Pred. No. 2.9e-291;
Matches 1347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 CTGGCAGTCCCGCTTCGAGAAATCAATCCAGTTTCGATACGGTCGATCAGGGGTATCAA 63
DB 58 CTGGCAGTCCCGCTTCGAGAAATCAATCCAGTTTCGATACGGTCGATCAGGGGTATCAA 117
QY 64 TCCTTCTCGAGACTTCGATCTTTGGGTCAATACGACACCGTTCTTCTCTGCGCAAC 123
DB 118 TCCTTCTCGAGACTTCGATCTTTGGGTCAATACGACACCGTTCTTCTCTGCGCAAC 177
QY 124 GAATCGGTCAATCTCCCTGAGGTGCCCGCGGATGATGATGATGATGATGATGATGAT 183
DB 178 GAATCGGTCAATCTCCCTGAGGTGCCCGCGGATGATGATGATGATGATGATGATGAT 237
QY 184 TCCGCTCATGGAGCGGTATCCGACCGACTCCAGGCGCAAGAAATATCGCTCTCAATT 243
DB 238 TCCGCTCATGGAGCGGTATCCGACCGACTCCAGGCGCAAGAAATATCGCTCTCAATT 297
QY 244 GAGGAGATCCAGCAAGACGCGACCACTTTGACGAAATATGCTTCTGAGACATAC 303
DB 298 GAGGAGATCCAGCAAGACGCGACCACTTTGACGAAATATGCTTCTGAGACATAC 357
QY 304 AACTCAGTTGGGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 363
DB 358 AACTCAGTTGGGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 417
QY 364 GGCATCAAGTTCTACGAGCGGTACGAATCGCTCAAGGAAATATGCTTCTCAATCCGA 423
DB 418 GGCATCAAGTTCTACGAGCGGTACGAATCGCTCAAGGAAATATGCTTCTCAATCCGA 477
QY 424 TCCTTGGCTTCAGCGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 483
DB 478 TCCTTGGCTTCAGCGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 537
QY 484 ACCAAGCTGAAGGATCTCGTCCGACCGCGCAATCGTCCGCAAGATGATGATGATGATGAT 543
DB 538 ACCAAGCTGAAGGATCTCGTCCGACCGCGCAATCGTCCGCAAGATGATGATGATGATGAT 597
QY 544 ATTTCCAGGCGAGCTCATTCACCAACTCTCGACCCAGGCACTGCTGCTCTCGAA 603
DB 598 ATTTCCAGGCGAGCTCATTCACCAACTCTCGACCCAGGCACTGCTGCTCTCGAA 657
QY 604 GACAGCAATTTGGCGGATACCGTTCGAAGCAATTTACCGCCACGTTTCCTCCCTCAAT 663
DB 658 GACAGCAATTTGGCGGATACCGTTCGAAGCAATTTACCGCCACGTTTCCTCCCTCAAT 717
QY 664 CGTCAAGCTTCGAGAAACGACTGTCGCGGTGATCTCTCACAGACACAGAAAGTGAAGTAC 723
DB 718 CGTCAAGCTTCGAGAAACGACTGTCGCGGTGATCTCTCACAGACACAGAAAGTGAAGTAC 777
QY 724 CTCAATGACATGTCTCTTTCGACCACTCTCCACAGCACCGTTCGACACCAAGCTGTCC 783
DB 778 CTCAATGACATGTCTCTTTCGACCACTCTCCACAGCACCGTTCGACACCAAGCTGTCC 837
QY 784 CCCTTCTGTGACCTGTTCACCCATGACGAATGGAATCAACTACGATACCTCCAGTCTTG 843

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Db      838  CCCTTCTGTGACCTGTTACCCATGACGAATGAGTCACTACGACTACCTCCAGTCTCTG  897
Qy      844  AAAAAAGTATTACGGCCATGTTGTCAGGTAAACCGGTTCGGCCCGACCCAGGGCGTTCGGCTAC  903
Db      898  AAAAAAGTATTACGGCCATGTTGTCAGGTAAACCGGTTCGGCCCGACCCAGGGCGTTCGGCTAC  957
Qy      904  GTTAACGAGCTCATCGCCCGTCTGACCCACTCGCTGTCACGATGCCAGATGACACAGTTCACAAC  963
Db      958  GCTAACGAGCTCATCGCCCGTCTGACCCACTCGCTGTCACGATGCCAGATGACACAGTTCACAAC  1017
Qy      964  CACACTTTGGACTCGAGCCCGGCTACCTTTCCGCTCAACTCTACTCTCTACCGGACTTTT  1023
Db      1018  CACACTTTGGACTCGAGCCCGGCTACCTTTCCGCTCAACTCTACTCTCTACCGGACTTTT  1077
Qy      1024  TCGCATGACAAACGGCATCATCTCCATTTCTTTTGTAGGTCTGTACAAAGGCACTAAG  1083
Db      1078  TCGCATGACAAACGGCATCATCTCCATTTCTTTTGTAGGTCTGTACAAAGGCACTAAG  1137
Qy      1084  CCGCTATCTACACGACCGTGGAGAAATATCACCCAGACAGATGGATTCTCGTCTGCTTGG  1143
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Qy      1204  CCGCTGGTCCGTTGCTTAAATGATCGCGTGTGTCGCGTGTGATCGGTTGAT  1263
Db      1258  CCGCTGGTCCGTTGCTTAAATGATCGCGTGTGTCGCGTGTGATCGGTTGAT  1317
Qy      1264  GCTTTGGGGAGATGACCCGGATAGCTTTGTGAGGGGGTTGAGCTTTGCTAGACTGGG  1323
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Qy      1324  GGTGATTGGCGGAGTGTTTGGCTTAG  1350
Db      1378  GGTGATTGGCGGAGTGTTTGGCTTAG  1404

RESULT 4
LOCUS      AR195149                      1404 bp      DNA      linear      PAT 20-APR-2002
DEFINITION Sequence 33 from patent US 6350602.
ACCESSION  AR195149
VERSION     AR195149.1  GI:20244586
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 1404)
AUTHORS   Van Gorcom,R.F.M., Van Hartingsveldt,W., Van Paridon,P.Andreas.,
Veenstra,A.Eveline., Luiten,R.G.M. and Seiten,G.C.M.
TITLE      Cloning and expression of phytase from aspergillus
JOURNAL    Patent: US 6350602-A 33 26-FEB-2002;
FEATURES   Location/Qualifiers
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ORIGIN
Query Match      99.8%; Score 1347; DB 6; Length 1404;
Best Local Similarity 100.0%; Pred. No. 2,9e-291;
Matches 1347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4  CTGCAGTCCCGCTCGAGAAATCAATCCAGTTCGATACGGTTCGATCAGGGGTATCAA  63
Db      58  CTGCAGTCCCGCTCGAGAAATCAATCCAGTTCGATACGGTTCGATCAGGGGTATCAA  117
Qy      64  TGCTTCTCCGAGACTTCGCATCTTTGGGTCAATACGACCGTTCCTCTCTGCGCAAC  123
Db      118  TGCTTCTCCGAGACTTCGCATCTTTGGGTCAATACGACCGTTCCTCTCTGCGCAAC  177
Qy      124  GAATCGGTATCTCCCTGAGGTGCCCGCGGATGACAGATCACTTTGCGTCAAGTCTC  183
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Db      238  TCCGTCATGGAGCGGTATCCGACCGACTCAAAGGCAAGAAATACTCCGCTCTCAAT  297
Qy      244  GAGGATCCAGACAGAACGGACACCTTTGACGGAATAATGCTTCTCTGAGACATAC  303
Db      298  GAGGATCCAGACAGAACGGACACCTTTGACGGAATAATGCTTCTCTGAGACATAC  357
Qy      304  AACTACAGCTTGGGTGACAGATGACCTGCTCCCTTCGGAGAACAGAGTAGTCAACTCC  363
Db      358  AACTACAGCTTGGGTGACAGATGACCTGCTCCCTTCGGAGAACAGAGTAGTCAACTCC  417
Qy      364  GGCATCAAGTTCTACAGCGGTACGAATCGTTCACAGAACATGTTCCATTCGGA  423
Db      418  GGCATCAAGTTCTACAGCGGTACGAATCGTTCACAGAACATGTTCCATTCGGA  477
Qy      424  TCCTCTGGCTCCAGCGGTGATCGCTCCCGCAAGAAATTCATCGAGGGTTCAGAGC  483
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Qy      484  ACCAAGCTGAAGGATCTCTGTCGCCAGCCCGGCCAATCGTCCGCAAGATCGAGTGTG  543
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Qy      544  ATTTCCGAGGCCAGTCTCATCAACAACTCTCGACCCAGCACCTGACACTGTCTCGAA  603
Db      598  ATTTCCGAGGCCAGTCTCATCAACAACTCTCGACCCAGCACCTGACACTGTCTCGAA  657
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Qy      664  CGTCAACGTCTGGAGAACGACCTGTCGGTGTGACTCTCAGACACACAGAGTGCCTAC  723
Db      718  CGTCAACGTCTGGAGAACGACCTGTCGGTGTGACTCTCAGACACACAGAGTGCCTAC  777
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Qy      784  CCCTTCTGTGACCTGTTACCCGATGACGAATGGATCAACTACGACTACCTCCAGTCTTG  843
Db      838  CCCTTCTGTGACCTGTTACCCGATGACGAATGGATCAACTACGACTACCTCCAGTCTTG  897
Qy      844  AAAAAAGTATTACGGCCATGTTGTCAGGTAAACCGGTTCGGCCCGACCCAGGGCGTTCGGCTAC  903
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Qy      904  GCTAACGAGCTCATCGCCCGTCTGACCCACTCGCTGTCACGATGCCAGTTCACAAC  963
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Db      1018  CACACTTTGGACTCGAGCCCGGCTACCTTTCCGCTCAACTCTACTCTCTACCGGACTTT  1077
Qy      1024  TCGCATGACAAACGGCATCATCTCCATTTCTTTTGTAGGTCTGTACAAAGGCACTAAG  1083
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Qy      1144  ACGGTTCCGTTTGTCTTCGCGTTTGTAGTCGAGATGATGCAAGTGTAGGGGGAGCAGGAG  1203
Db      1198  ACGGTTCCGTTTGTCTTCGCGTTTGTAGTCGAGATGATGCAAGTGTAGGGGGAGCAGGAG  1257
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Qy 1324 GGTGATTCGGCGGAGTGTGTTTGCCTTAG 1350
Db 1378 GGTGATTCGGCGGAGTGTGTTTGCCTTAG 1404

RESULT 5
LOCUS ANPHYAG 2000 bp DNA linear PLN 24-MAY-2004
DEFINITION Aspergillus niger phyA gene.
ACCESSION Z16414
VERSION Z16414.1 GI:2392
KEYWORDS phyA gene.
SOURCE Aspergillus niger
ORGANISM Aspergillus niger
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
van Hartingsveldt, W., Van Zeijl, C.M.J., Harteveld, M.G., Gouka, R.J.,
Suykerbuyk, M.E.G., Luitzen, R.G.M., Van Paridon, P.A., Sellen, G.C.M.,
Veenstra, A.E., Van Gorcom, R.F.M., and Van Den Hondel, C.A.M.J.
Cloning, molecular characterization and overexpression of the
phyAase gene (phyA) of Aspergillus niger
Gene (1992) In press
2 (bases 1 to 2000)
van Hartingsveldt, W.
Direct Submission
Submitted (05-OCT-1992) Van Hartingsveldt W., TNO Medical
Biological Laboratory, Lange Kleiweg 139, Rijswijk, the Netherlands
LOCATION/Qualifiers
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166..1871
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166..253
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sig_peptide
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intron
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ORIGIN
Query Match 99.8%; Score 1347; DB 8; Length 2000;
Best Local Similarity 100.0%; Pred. No. 2.9e-291;
Matches 1347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 CTGGCAGTCCCGCCTCGAGAAATCAATCCAGTTCGGATACGGTCGATCAGGGGTATCAA 63
Db 369 CTGGCAGTCCCGCCTCGAGAAATCAATCCAGTTCGGATACGGTCGATCAGGGGTATCAA 428
Qy 64 TGCTTCTCCGAGACTTCGCATCTTTGGGGTCAATACGCACCGTTCCTCTCTCTGGCAAAAC 123
Db 429 TGCTTCTCCGAGACTTCGCATCTTTGGGGTCAATACGCACCGTTCCTCTCTCTGGCAAAAC 488
Qy 124 GAATCGGTCAATCTCCCTGAGGTGCCCGCGGATGCAGAGTCACTTTTGGCTCAGGTCTTC 183
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 1 (bases 1 to 2665)
 Mullaney, E.J., Gibson, D.M. and Ullah, A.H.
 Positive identification of a lambda gt11 clone containing a region
 of fungal phytase gene by immunoprobe and sequence verification
 Appl. Microbiol. Biotechnol. 35 (5), 611-614 (1991)
 JOURNAL 9200601
 MEDLINE 1369340
 PUBMED
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 JOURNAL Unpublished (1992)
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AUTHORS Van Gorcom,R.P.M., Van Hartingsveldt,W., Van Paridon,P.A.,
Veenstra,A.E., Luiten,R.G.M. and Sellen,G.C.M.
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AUTHORS	Van Gormom, R.F.M., Van Hartingsveldt, W., Van Paridon, P. Andreas., Veenstra, A. Eveline., Luiten, R.G.M. and Selten, G.C.M.		
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DEFINITION	Sequence 7 from patent US 5780292.		
ACCESSION	AR018076		
VERSION	AR018076.1 GI:3973679		
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 2363)		
AUTHORS	Nevalainen, H.K.M., Paloheimo, M.T., Miettinen-Oinonen, A.S.K., Torkkeli, T.K., Cantrell, M., Piddington, C.S., Rambosek, J.A., Turunen, M.K. and Fagerstrom, R.B.		

TITLE Production of phytate degrading enzymes in trichoderma
JOURNAL Patent: US 5780292-A 7 14-JUL-1998;
FEATURES Location/Qualifiers

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ORIGIN

Query Match 94.4%; Score 1275; DB 6; Length 2363;
Best Local Similarity 96.7%; Pred. No. 4e-275;
Matches 1302; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

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DB 803 GAGGAGTCCAGCAAGACGACCACTTTGACGGAAATATGCTTCTCTGAAGACATAC 862
QY 304 AACTACAGCTTGGGTGAGATGACCTGACTCCCTTCGGAGAAAGAGTGTCAATCC 363
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RESULT 11

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LOCUS
DEFINITION Sequence 7 from patent US 5830733.
ACCESSION AR051916
VERSION AR051916.1 GI:5975280
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2363)
AUTHORS Nevalainen,H.K.M., Paloheimo,M.T., Miettinen-Oinonen,A.S.K.,
Torckeli,T.K., Cantrell,M., Piddington,C.S., Rambossek,J.A.,
Turunen,M.K., Fagerstrom,R.B. and Houston,C.S.
TITLE Nucleic acid molecules encoding phytase and ph2.5 acid phosphatase
JOURNAL Patent: US 5830733-A 7 03-NOV-1998;
FEATURES Location/Qualifiers
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ORIGIN

Query Match 94.4%; Score 1275; DB 6; Length 2363;
Best Local Similarity 96.7%; Pred. No. 4e-275;
Matches 1302; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
QY 4 CTGGCAGTCCCGCTCGAGAAATCAATCCAGTTCGCGATACGGTCGATCAGGGGTATCAA 63
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RESULT 14
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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Aspergillus niger strain N14* phytase (phyA) gene, complete cds.
AY426977.1 GI:38018638
Aspergillus niger
Aspergillus niger
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

1 (bases 1 to 1525)
Peng,Y.Y., Zhou,Z.Y. and Ma,L.P.
Cloning and characterization of phytase gene of Aspergillus niger
N14*
Unpublished
2 (bases 1 to 1525)
Peng,Y.Y., Zhou,Z.Y. and Ma,L.P.
Direct Submission
Submitted (01-OCT-2003) College of Animal Science & Technology,
Southwest Agricultural University, Hiansheng, Beibei, Chongqing
400716, P.R. China
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ORIGIN

Query Match	94.1%;	Score 1270.2;	DB 8;	Length 1525;	
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 precursor, gene, complete cds.
 ACCESSION AF218813
 VERSION AF218813.1 GI:6694940
 KEYWORDS
 SOURCE Aspergillus niger

Aspergillus niger
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 1 (bases 1 to 1528)
 Hongning, W., Qi, W. and Jing, X.
 PCR, cloning and characterization of the phytase (phyA) gene of
 Aspergillus niger (China Strain)
 Unpublished
 2 (bases 1 to 1528)
 Hongning, W., Qi, W. and Jing, X.
 Title Submission
 Submitted (24-DEC-1999) Aniaml Sci. & Tech. College, Sichuan
 Agricultural University, Ya'an City, Sichuan Province 625014,
 P.R.China

Location/Qualifiers
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Query Match 94.0%; Score 1268.6; DB 8; Length 1528;
 Best Local Similarity 96.4%; Pred No. 1.1e-273;
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Qy 904 GCTAACGAGCTCATCGCCCGCTGACCCACTCGCCTGTCCACGATGACACCAAGTTCACAC 963
Db 1073 GCTAACGAGCTCATCGCCCGCTGACCCACTCGCCTGTCCACGATGACACCAAGTTCACAC 1132
Qy 964 CACACTTTGGACTCGGCCGGCTACCTTTCCGCTCAACTCTACTCTCTACGGGACTTT 1023
Db 1133 CACACATTTGGACTCTAATCGGCTACCTTTCCGCTCAACTCTACTCTCTACGGGACTTT 1192
Qy 1024 TCGCATGACACAGGCATCATCTCCATTCCTTTGCTTTAGGTCGTGTACAAACGGCCTAAG 1083
Db 1193 TCCACGATTAACGGCATCATCTCTATTCTCTTTGCTTTGGGTCTGTATTAACGGCACCAAG 1252
Qy 1084 CCGCTATCTACACGACGCTGGAGAAATACCCAGACAGATGGATTCGTCTGCTTGG 1143
Db 1253 CCGCTGTCTACACGACGCTGCAGAAATACCCAGACAGATGGATTCGTCTGCTTGG 1312
Qy 1144 ACGGTTCCGTTTGTCTCGCGTTTGTAGCTCGAGATGATCGAGTGTAGGGCGGAGCAGGAG 1203
Db 1313 ACGGTTCCGTTTGTCTCGCGTTTGTAGCTCGAGATGATCGAGTGTAGGGCGGAGCAGGAG 1372
Qy 1204 CCGCTGCTCCGTTGCTTTGGTTAATGATCGGTTTCTCCGCTGCATGGGTGTCCGGTTGAT 1263
Db 1373 CCGCTGCTCCGTTGCTTTGGTTAATGATCGGTTTCTCCGCTGCATGGGTGTCCGGTTGAT 1432
Qy 1264 GCTTTGGGGATGTACCCGGGATAGCTTTGTAGGGGGTTGAGCTTTGCTAGATCTGGG 1323
Db 1433 GCTTTAGGGGATGTACCCGGGATAGCTTTGTAGGGGGTTGAGCTTTGCTAGATCTGGG 1492
Qy 1324 GGTGATTGGCGGAGTGTTTTGCTTAG 1350
Db 1493 GGTGATTGGCGGAGTGTTTTGCTTAG 1519
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Search completed: November 24, 2004, 09:38:29
Job time : 6032 secs

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OM nucleic - nucleic search, using sw model

Run on: November 24, 2004, 06:11:07 ; Search time 728 Seconds
(without alignments)
9734.503 Million cell updates/sec

Title: US-10-089-364-3

Perfect score: 1350

Sequence: 1 atgtgtgcagtcctccgcctc.....gggcggagtgtttgcctag 1350

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_23Sep04.*

1: Geneseq1980s.*

2: Geneseq1990s.*

3: Geneseq2000s.*

4: Geneseq2001as.*

5: Geneseq2001bs.*

6: Geneseq2002as.*

7: Geneseq2002bs.*

8: Geneseq2003as.*

9: Geneseq2003bs.*

10: Geneseq2003cs.*

11: Geneseq2003ds.*

12: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1350	100.0	1350	4 AAD03283	Aad03283 Aspergill
2	1350	100.0	1449	4 AAD03287	Aad03287 Carrot ex
3	1347	99.8	1404	2 AAQ11175	Aaql1175 Chromosom
4	1347	99.8	1404	2 AAZ27421	Aaz27421 A. ficcum
5	1347	99.8	1506	6 ABN85588	Abn85588 Aspergill
6	1347	99.8	2665	12 ADL91241	Adl91241 Wild-type
7	1347	99.8	6756	2 AAQ11174	Aaql1174 Sequence,
8	1347	99.8	6756	2 AAT65137	Aat65137 Aspergill
9	1347	99.8	6756	8 ABX13436	Abx13436 Plasmids
10	1345.4	99.7	1404	2 AAT65136	Aat65136 Aspergill
11	1345.4	99.7	2665	12 ADL91263	Adl91263 Mutant ph
12	1345.4	99.7	2665	12 ADL91267	Adl91267 Mutant ph
13	1345.4	99.7	2665	12 ADL91247	Adl91247 Mutant ph
14	1345.4	99.7	2665	12 ADL91251	Adl91251 Mutant ph
15	1345.4	99.7	2665	12 ADL91259	Adl91259 Mutant ph
16	1345.4	99.7	2665	12 ADL91257	Adl91257 Mutant ph
17	1345.4	99.7	2665	12 ADL91269	Adl91269 Mutant ph
18	1345.4	99.7	2665	12 ADL91265	Adl91265 Mutant ph
19	1345.4	99.7	2665	12 ADL91273	Adl91273 Mutant ph
20	1345.4	99.7	2665	12 ADL91245	Adl91245 Mutant ph
21	1345.4	99.7	2665	12 ADL91261	Adl91261 Mutant ph

22	1343.8	99.5	1404	2 AAQ13878	Aaql3878 Phytase g
23	1343.8	99.5	2665	12 ADL91308	Adl91308 Mutant ph
24	1343.8	99.5	2665	12 ADL91281	Adl91281 Mutant ph
25	1343.8	99.5	2665	12 ADL91255	Adl91255 Mutant ph
26	1343.8	99.5	2665	12 ADL91271	Adl91271 Mutant ph
27	1343.8	99.5	2665	12 ADL91279	Adl91279 Mutant ph
28	1343.8	99.5	2665	12 ADL91275	Adl91275 Mutant ph
29	1342.4	99.4	1344	6 ABN85591	Abn85591 Aspergill
30	1342.2	99.4	2665	12 ADL91277	Adl91277 Mutant ph
31	1342.2	99.4	2665	12 ADL91291	Adl91291 Mutant ph
32	1342.2	99.4	2665	12 ADL91283	Adl91283 Mutant ph
33	1342.2	99.4	2665	12 ADL91289	Adl91289 Mutant ph
34	1342.2	99.4	2665	12 ADL91285	Adl91285 Mutant ph
35	1340.6	99.3	2665	12 ADL91293	Adl91293 Mutant ph
36	1340.6	99.3	2665	12 ADL91287	Adl91287 Mutant ph
37	1337.4	99.1	2665	12 ADL91295	Adl91295 Mutant ph
38	1275	94.4	2363	2 AAQ58126	Aaq58126 Phytase g
39	1275	94.4	2379	2 AAQ56944	Aaq56944 A. niger
40	1185.4	87.8	1590	12 ADK90935	Adk90935 Aspergill
41	1182	87.6	1350	4 AAD03282	Aad03282 Aspergill
42	1182	87.6	1449	4 AAD03286	Aad03286 Carrot ex
43	1166.2	86.4	1515	2 AAT96709	Aat96709 Aspergill
44	1152.6	85.4	1335	12 ADL43256	Adl43256 Modified
45	1119	82.9	1335	12 ADL43254	Adl43254 Modified

ALIGNMENTS

RESULT 1
AAD03283
ID AAD03283 standard; DNA; 1350 BP.
XX
AC AAD03283;
XX
DT 13-JUN-2001 (first entry)
XX
DE Aspergillus niger phytase (Phy) A-1 gene.
XX
KW Phytase A; Phy; plant productivity; phosphorus utility;
KW biomass production; hypocotyl production; epicotyl production;
KW transgenic plant; phytate; ds.
XX
OS Aspergillus niger.
XX
FH Key Location/Qualifiers
CDS
FT 1..1350
FT /*tag= a
FT /product= "Aspergillus niger phytase A-1 protein"
XX
PN WO200122806-A1.
XX
PD 05-APR-2001.
XX
PF 22-SEP-2000; 2000WO-AU001183.
XX
PR 24-SEP-1999; 99AU-00003049.
XX
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
PA (AUMO-) AUSTRALIAN WOOL RES & PROMOTION ORG.
XX
PI Richardson AE, Hayes JE, Simpson RJ;
DR WPI: 2001-244964/25.
DR P-PSDB; AAY72974.
XX
PT New isolated nucleic acid encoding a mature phytase polypeptide for
PT enhancing the phosphorus nutrition of a plant, the growth of a plant on a
PT phosphorus source and the phosphorus content of a plant.
XX
PS Claim 7; Page 121-124; 144pp; English.
XX
CC The invention relates to a method of modifying plant productivity which

CC involves expressing phytase (Phy) A gene from *Aspergillus niger* in a
CC plant cell. Phytase gene is capable of facilitating plants ability to
CC utilise soil phosphorus. It is used to enhance the phosphorus nutrition
CC of a plant or the growth of a plant on a phosphorus source comprising
CC phytate and/or increase the phosphorus content of a plant. This gene is
CC used to enhance the biomass produced by a plant and also to enhance the
CC rate of hypocotyl production or the rate of epicotyl production.
CC Transgenic plant containing phytase gene has improved productivity than
CC its isogenic counterparts. The present sequence is *Aspergillus niger* Phy
CC A-1 gene. This gene is modified (Phy A-2 gene) in order to bring about
CC suitable expression in plant cells
XX
SQ Sequence 1350 BP; 288 A; 419 C; 332 G; 311 T; 0 U; 0 Other;

Query Match 100.0%; Score 1350; DB 4; Length 1350;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTGGCAGTCCCGCTCGAGAAATCAATCCAGTTGCGATACGGTTCGATCAGGGGTAT 60
DB 1 ATGCTGGCAGTCCCGCTCGAGAAATCAATCCAGTTGCGATACGGTTCGATCAGGGGTAT 60

QY 61 CAATGCTTCTCGAGACTTCGATCTTTGGGGTCAATACGACCGTTCCTCTCTCGCA 120
DB 61 CAATGCTTCTCGAGACTTCGATCTTTGGGGTCAATACGACCGTTCCTCTCTCGCA 120

QY 121 AACGAATCGGTTCATCTCCCTGAGTGCCTCCCGGATGCGAGTCACTTCGCTCAGGTC 180
DB 121 AACGAATCGGTTCATCTCCCTGAGTGCCTCCCGGATGCGAGTCACTTCGCTCAGGTC 180

QY 181 CTCTCCCTCATGAGCGCGTATCCGACCGACTCCAAAGGCAAGAAATCTCCGCTCTC 240
DB 181 CTCTCCCTCATGAGCGCGTATCCGACCGACTCCAAAGGCAAGAAATCTCCGCTCTC 240

QY 241 ATTGAGGAGTCCAGCAACCGCACCACTTTCGCGAATAATGCTTCTCTGAAGACA 300
DB 241 ATTGAGGAGTCCAGCAACCGCACCACTTTCGCGAATAATGCTTCTCTGAAGACA 300

QY 301 TACAACTACAGTTGGGTGCAGATGACCTGATCCCTTCGGAGAACAGGAGTCTCAAC 360
DB 301 TACAACTACAGTTGGGTGCAGATGACCTGATCCCTTCGGAGAACAGGAGTCTCAAC 360

QY 361 TCCGCGATCAAGTTCTACAGGGTACGAATCGTCTCAAGGACATCGTTCCATTCTC 420
DB 361 TCCGCGATCAAGTTCTACAGGGTACGAATCGTCTCAAGGACATCGTTCCATTCTC 420

QY 421 CGATCTCTGGCTCCAGCGCGGTGATCGCTCCGGCAAGAAATTCATCGAGGGCTTCCAG 480
DB 421 CGATCTCTGGCTCCAGCGCGGTGATCGCTCCGGCAAGAAATTCATCGAGGGCTTCCAG 480

QY 481 AGCAACAAGCTGAAGATCTCTGTCGCGAGCGCGCAATCGTCCGCCAAGATCGAGTG 540
DB 481 AGCAACAAGCTGAAGATCTCTGTCGCGAGCGCGCAATCGTCCGCCAAGATCGAGTG 540

QY 541 GTCAATTCGGAGCCAGTCTCAACAACTCTCGACCCAGGCACTGCACTGTCTTC 600
DB 541 GTCAATTCGGAGCCAGTCTCAACAACTCTCGACCCAGGCACTGCACTGTCTTC 600

QY 601 GAAGACAGCAATTCGGCGGATACCGTTCGAAGCCAAATTCACCGCAAGTTTCGTCCTCC 660
DB 601 GAAGACAGCAATTCGGCGGATACCGTTCGAAGCCAAATTCACCGCAAGTTTCGTCCTCC 660

QY 661 ATTCTGTCAGCTCTGGAGACGACCTGTCCGGTGTGACTCTCAGACACAGAGTGAAC 720
DB 661 ATTCTGTCAGCTCTGGAGACGACCTGTCCGGTGTGACTCTCAGACACAGAGTGAAC 720

QY 721 TACCTCATGGACATGTCTCTCGACACCATCTCCACGACCGTTCGACACCAAGCTG 780
DB 721 TACCTCATGGACATGTCTCTCGACACCATCTCCACGACCGTTCGACACCAAGCTG 780

QY 781 TCCCTCTGTGACTGTCTCCCTGACCAATGATCACTACGACTACCTCAGTCC 840
DB 781 TCCCTCTGTGACTGTCTCCCTGACCAATGATCACTACGACTACCTCAGTCC 840

QY 841 TTGAAAGTATTACGGCATGTGTCAGTAACCGCTCGGCCGACCCAGGGCTCGGC 900
DB 841 TTGAAAGTATTACGGCATGTGTCAGTAACCGCTCGGCCGACCCAGGGCTCGGC 900

QY 901 TAGCTTAACAGCTCATCGCCGTCTGACCCACTCGCTGTCCAGATGACACAGTTCC 960
DB 901 TAGCTTAACAGCTCATCGCCGTCTGACCCACTCGCTGTCCAGATGACACAGTTCC 960

QY 961 AACCACTTTGGAATTCGAGCCCGCTACCTTTCCGCTCAACTCTACTCTCTACCGGAC 1020
DB 961 AACCACTTTGGAATTCGAGCCCGCTACCTTTCCGCTCAACTCTACTCTCTACCGGAC 1020

QY 1021 TTTTTCGATGACAAAGGATCATCTCCATTTCTTTTGTGTTAGTCTGTACAAAGGCACT 1080
DB 1021 TTTTTCGATGACAAAGGATCATCTCCATTTCTTTTGTGTTAGTCTGTACAAAGGCACT 1080

QY 1081 AAGCGCTATCTACCAAGACCGTGGAGAAATATCACCGACAGATGGAATTTCTCTGCT 1140
DB 1081 AAGCGCTATCTACCAAGACCGTGGAGAAATATCACCGACAGATGGAATTTCTCTGCT 1140

QY 1141 TGGACGGTTCCGTTTGTTCGGGTTGTACGTGAGATGATGCACTGTTCAGGCGAGCAG 1200
DB 1141 TGGACGGTTCCGTTTGTTCGGGTTGTACGTGAGATGATGCACTGTTCAGGCGAGCAG 1200

QY 1201 GAGCGCTGCTCGGTCTTGTGTTAATGATCGGTTGTCCGCTGCATGGGTGTCGGTT 1260
DB 1201 GAGCGCTGCTCGGTCTTGTGTTAATGATCGGTTGTCCGCTGCATGGGTGTCGGTT 1260

QY 1261 GATGCTTTGGGAGATGATACCGGATAGCTTTGTGAGGGGTTGAGCTTTGCTAGATCT 1320
DB 1261 GATGCTTTGGGAGATGATACCGGATAGCTTTGTGAGGGGTTGAGCTTTGCTAGATCT 1320

QY 1321 GGGGGTGAATGGCGGAGTGTTCCTTAG 1350
DB 1321 GGGGGTGAATGGCGGAGTGTTCCTTAG 1350

RESULT 2
AAD03287
ID AAD03287 standard; DNA; 1449 BP.
XX
AC AAD03287;
XX
DT 11-SEP-2003 (revised)
DT 13-JUN-2001 (first entry)
XX
DE Carrot extensin leader peptide-A. niger phytase A-1 chimeric gene.
XX
KW Phytase A; Phy; plant productivity; phosphorus utility;
KW biomass production; hypocotyl production; epicotyl production;
KW transgenic plant; phytate; carrot; extensin; ds.
XX
OS *Daucus carota*.
OS *Aspergillus niger*.
OS Chimeric.
Key Location/Qualifiers
CDS 1..1449
FT /tag= a
FT /product= "Carrot extensin leader peptide-A. niger
FT phytase A-1 chimeric protein"
FT 1..100
FT /tag= b
FT /notes "Carrot extensin leader peptide"
FT 101..1446
FT /tag= c
FT /product= "Mature carrot extensin leader peptide- A.
FT niger phytase A-1 chimeric protein"
XX
PN WO200122806-A1.
XX
XX 05-APR-2001.

XX	22-SEP-2000; 2000WO-AU001183.	Db	580	AGCACCAAGCTGAAGGATCCTCGTGCCACGCGGCCAAATCGTCGCCCAAGATCGACGTC	639
PF					
XX	24-SEP-1999; 99AU-00003049.	Qy	541	GTCAATTTCCGAGGCCAGCTCATCCAAACAACATCTCTCGACCCAGGACCTGCACTGCTCTTC	600
PR					
XX	(CSIR) COMMONWEALTH SCI & IND RES ORG.	Db	640	GTCAATTTCCGAGGCCAGCTCATCCAAACAACATCTCTCGACCCAGGACCTGCACTGCTCTTC	699
PA	(AUWO-) AUSTRALIAN WOOL RES & PROMOTION ORG.	Qy	601	GAAGACAGCGAAATGGCCGATACCGTCGAAGCAATTTTCAACGCCACGTTGCTCCCTCC	660
XX		Db	700	GAAGACAGCGAAATGGCCGATACCGTCGAAGCAATTTTCAACGCCACGTTGCTCCCTCC	759
PI	Richardson AE, Hayes JE, Simpson RJ;	Qy	661	ATTGCTCAACGCTGGAGAACGACCTGTCGGGTGTGACTCTCACAGACACAGAGTGACC	720
XX		Db	760	ATTGCTCAACGCTGGAGAACGACCTGTCGGGTGTGACTCTCACAGACACAGAGTGACC	819
DR	WPI; 2001-244964/25.	Qy	721	TACCTCATGACACATGTGCTCTTCCGACACCATCTCCACGACGACCGTCGACACCAAGCTG	780
PT	New isolated nucleic acid encoding a mature phytase polypeptide for	Db	820	TACCTCATGACACATGTGCTCTTCCGACACCATCTCCACGACGACCGTCGACACCAAGCTG	879
PT	enhancing the phosphorus nutrition of a plant, the growth of a plant on a	Qy	781	TCCCTCTCTGTGACCTGTTTCAACCATGAGAAATGATCACTACGACTACCTCCAGTCC	840
PT	phosphorus source and the phosphorus content of a plant.	Db	880	TCCCTCTCTGTGACCTGTTTCAACCATGAGAAATGATCACTACGACTACCTCCAGTCC	939
XX	Claim 9; Fig 1; 144pp; English.	Qy	841	TTGAAAAGATTTACGCGCCATGTGTCAGGTAAACCGCTCGGCCGACCCAGGCGCTCGGC	900
PS		Db	940	TTGAAAAGATTTACGCGCCATGTGTCAGGTAAACCGCTCGGCCGACCCAGGCGCTCGGC	999
XX	The invention relates to a method of modifying plant productivity which	Qy	901	TACGCTAAACGAGCTATACGCGCTGTGACCCCATCGCTGTCCAGATGACACCAAGTTC	960
CC	involves expressing phytase (Phy) A gene from <i>Aspergillus niger</i> , in a	Db	1000	TACGCTAAACGAGCTATACGCGCTGTGACCCCATCGCTGTCCAGATGACACCAAGTTC	1059
CC	plant cell. Phytase gene is capable of facilitating plants ability to	Qy	961	AACCAACATTTGGACTCGAGCCGCGCTACTCTTCGCTCAACTCTACTCTCTACCGGGAC	1020
CC	utilise soil phosphorus. It is used to enhance the phosphorus nutrition	Db	1060	AACCAACATTTGGACTCGAGCCGCGCTACTCTTCGCTCAACTCTACTCTCTACCGGGAC	1119
CC	of a plant or the growth of a plant on a phosphorus source comprising	Qy	1021	TTTTGCGATGACAAACGSCATCATCTCCATTCTCTTTTGGTCTGTACACGSCACT	1080
CC	phytase and/or increase the phosphorus content of a plant. This gene is	Db	1120	TTTTGCGATGACAAACGSCATCATCTCCATTCTCTTTTGGTCTGTACACGSCACT	1179
CC	used to enhance the biomass produced by a plant and also to enhance the	Qy	1081	AAGCCGCTATCTACACGACCGTGGAGAAATATACCCAGACAGATGGATTCTCGTCTGCT	1140
CC	rate of hypocotyl production or the rate of epicotyl production.	Db	1180	AAGCCGCTATCTACACGACCGTGGAGAAATATACCCAGACAGATGGATTCTCGTCTGCT	1239
CC	Transgenic plant containing phytase gene has improved productivity than	Qy	1141	TGACCGGTTCCGTTTTCGTTTGTACGTCGAGATGATGACGTCGAGCGGACGAC	1200
CC	its isogenic counterparts. The present sequence is carrot extensin leader	Db	1240	TGACCGGTTCCGTTTTCGTTTGTACGTCGAGATGATGACGTCGAGCGGACGAC	1299
CC	peptide-A. <i>niger</i> phytase A-1 chimeric gene. This chimeric gene is used to	Qy	1201	GAGCCGCTGGTCCGTCCTTGTGTTAATGATCGGTTGTCGCCGTGCAATGGGTTCGGTT	1260
CC	enhance phosphorus nutrition in plants. (Updated on 11-SEP-2003 to	Db	1300	GAGCCGCTGGTCCGTCCTTGTGTTAATGATCGGTTGTCGCCGTGCAATGGGTTCGGTT	1359
CC	standardise OS field)	Qy	1261	GATGCTTTGGGAGATGATACCGGGATAGCTTTGTGAGGGGGTTGAGCTTTCTAGATCT	1320
XX		Db	1360	GATGCTTTGGGAGATGATACCGGGATAGCTTTGTGAGGGGGTTGAGCTTTCTAGATCT	1419
SEQ	Sequence 1449 BP; 312 A; 439 C; 355 G; 343 T; 0 U; 0 Other;	Qy	1321	GGGGGTGATTGGGCGGAGTGTGTTTTCCTTAG-1350	
	Query Match 100.0%; Score 1350; DB 4; Length 1449;	Db	1420	GGGGGTGATTGGGCGGAGTGTGTTTTCCTTAG-1449	
	Best Local Similarity 100.0%; Pred. No. 0;				
	Matches 1350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Qy	1 ATGTGGCAGTCCCGCTCGAGAAATCAATCCAGTTGCGATACGTCGATCAGGGGTAT 60				
Db	100 ATGTGGCAGTCCCGCTCGAGAAATCAATCCAGTTGCGATACGTCGATCAGGGGTAT 159				
Qy	61 CAATGCTTCTCGAGACTTCCATCTTTGGGGTCAATACGACCGTTCTCTCTCTCGCA 120				
Db	160 CAATGCTTCTCGAGACTTCCATCTTTGGGGTCAATACGACCGTTCTCTCTCTCGCA 219				
Qy	121 AACGAATCGGTATCTCCCTGAGGTGCCCGCGGATGCAGATCACTTTGCTCAGGTC 180				
Db	220 AACGAATCGGTATCTCCCTGAGGTGCCCGCGGATGCAGATCACTTTGCTCAGGTC 279				
Qy	181 CTCTCCGTCATGGAGCGGGTATCCGACGACTCCAGGGCAGAAATCTCGCTCTC 240				
Db	280 CTCTCCGTCATGGAGCGGGTATCCGACGACTCCAGGGCAGAAATCTCGCTCTC 339				
Qy	241 ATTGAGGAGATCCAGCAGAACCGACCACTTTTGACGGAAATATGCTTCTTCAAGACA 300				
Db	340 ATTGAGGAGATCCAGCAGAACCGACCACTTTTGACGGAAATATGCTTCTTCAAGACA 399				
Qy	301 TACAATCAGCTTGGGTGAGATGACCTGCTCCCTTCGAGAACAGGAGCTAGTCAAC 360				
Db	400 TACAATCAGCTTGGGTGAGATGACCTGCTCCCTTCGAGAACAGGAGCTAGTCAAC 459				
Qy	361 TCCGSCATCAAGTTCTACACGGGTACGAATCGGTCAACGAACATCGTTCCATTTCATC 420				
Db	460 TCCGSCATCAAGTTCTACACGGGTACGAATCGGTCAACGAACATCGTTCCATTTCATC 519				
Qy	421 CGATCTCTGCTCCAGCGGTCATCGCTCCCGGCAAGAAATTCATCGAGGGCTCCAG 480				
Db	520 CGATCTCTGCTCCAGCGGTCATCGCTCCCGGCAAGAAATTCATCGAGGGCTCCAG 579				
Qy	481 AGCACCAGCTGAAGGATCCTGTCGCCAGCGCGGCAATCGTCGCCCAAGATCGAGTG 540				

RESULT 3
AAQ11175
ID AAQ11175 standard; cDNA; 1404 BP.
XX
AC AAQ11175;
XX
XX 25-MAR-2003 (revised)
DT 30-MAR-2000 (revised)
DT 31-MAY-1991 (first entry)
XX
DE Chromosomal phytase encoding sequence.
XX
KW Microbial phytase; animal feed; inositol; inorganic phosphate; ss.
XX

Db 1318 GCTTTGGGAGATGATACCCGGATAGCTTTGTGAGGGGGTTGAGCTTTGTAGATCTGGG 1377
QY 1324 GGTGATTGGGGGAGTGTGTTTGCCTTAG 1350
Db 1378 GGTGATTGGGGGAGTGTGTTTGCCTTAG 1404

RESULT 5
ABN85588
ID ABN85588 standard; DNA; 1506 BP.
XX
AC ABN85588;
XX
DT 17-SEP-2002 (first entry)
XX
DE Aspergillus niger phyA related polynucleotide 2.
XX
KW Yeast; Aspergillus niger; phytase; phyA; Pasteur Pichia; gene; ds.
XX
OS Aspergillus niger.
XX
FH Key Location/Qualifiers
CDS 1..1506
FT /*tag= a
FT /product= "phyA related protein"
FT exon 1..44
FT /*tag= b
FT /number= 1
FT intron 45..146
FT /*tag= c
FT /number= 1
FT exon 147..1506
FT /*tag= d
FT /number= 2
XX
CN1333363-A.
XX
PN 30-JAN-2002.
XX
PF 12-JUL-2000; 2000CN-00117245.
XX
PR 12-JUL-2000; 2000CN-00117245.
XX
PA (RAIS-) INST RAISE LIVESTOCK GUANGDONG ACAD AGRI.
XX
PI Chen Z, Yang L, Fang L;
XX
DR WPI: 2002-305615/35.
DR P-P5DB; ABN83810.
XX
PT Phytase gene sequence and application in yeast thereof.
XX
PS Disclosure; Fig 1; 48pp; Chinese.
XX
CC The invention relates to a coded phytase gene sequence suitable for
CC secretion and expression in yeast and its application. It is mainly
CC characterised by removing nucleotide sequence of +45-+146 bit from phyA
CC total length structure gene sequence, removing Aspergillus niger signal
CC peptide coded sequence of +1-+44 and +147-+159, connecting a part of
CC signal peptide code sequence suitable for secretion and expression at 5'
CC end and connecting a restriction endonuclease site at 3' end. The
CC different carriers can be connected into said gene sequence so as to form
CC a recombinant plasmid with different functions and after the recombinant
CC plasmid using pPICZ alpha A as carrier is converted into Pasteur Pichia
CC yeast, finally the invented Pasteur Pichia yeast engineering bacterium
CC (CCTCC NO:M200005) can be obtained through the screening process. By
CC using the invention the industrial process of phytase bio-expression can
CC be successfully implemented. The present sequence is that of a
CC polynucleotide of the invention
XX
SQ Sequence 1506 BP; 318 A; 465 C; 369 G; 354 T; 0 U; 0 Other;
Query Match 99.8%; Score 1347; DB 6; Length 1506;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CTGGCAGTCCCGCCCTCGAGAAATCAATCCAGTTGCGATACGGTTCGATCAGGGGTATCAA 63
Db 160 CTGGCAGTCCCGCCCTCGAGAAATCAATCCAGTTGCGATACGGTTCGATCAGGGGTATCAA 219

QY 64 TGCTTCTCCGAGACTTGGGATCTTTGGGGTCAATACGACCGTTTCTTCTCTGCAAAAC 123
Db 220 TGCTTCTCCGAGACTTGGGATCTTTGGGGTCAATACGACCGTTTCTTCTCTGCAAAAC 279

QY 124 GAATCGGTCAATCCCTCGAGTGCCTCGCGGATCGAGTCACTTTGGCTCAGTCTCTC 183
Db 280 GAATCGGTCAATCCCTCGAGTGCCTCGCGGATCGAGTCACTTTGGCTCAGTCTCTC 339

QY 184 TCCGTCATGAGAGCGGATTCGACCGGATCCGACCGGATCCGAGGCAAGAAATCTCGCTCTCAT 243
Db 340 TCCGTCATGAGAGCGGATTCGACCGGATCCGACCGGATCCGAGGCAAGAAATCTCGCTCTCAT 399

QY 244 GAGGATCCAGCAGAACCGGACCACTTTGACGGAAATATGCTTCTCTGAAGACATAC 303
Db 400 GAGGATCCAGCAGAACCGGACCACTTTGACGGAAATATGCTTCTCTGAAGACATAC 459

QY 304 AACTACAGCTTGGGTGAGATGACCTGACTCCCTTCGAGAACAGGAGCTAGTCAACTCC 363
Db 460 AACTACAGCTTGGGTGAGATGACCTGACTCCCTTCGAGAACAGGAGCTAGTCAACTCC 519

QY 364 GGCATCAAGTTCTACAGGGGTACGAATCGCTCAAGAGAACATGTTCCATTCATCCGA 423
Db 520 GGCATCAAGTTCTACAGGGGTACGAATCGCTCAAGAGAACATGTTCCATTCATCCGA 579

QY 424 TCCTCTGGCTCCAGCGGGTGTGATCGCTCCGCGCAAGAAATTCATCGAGGGCTTCAGAGC 483
Db 580 TCCTCTGGCTCCAGCGGGTGTGATCGCTCCGCGCAAGAAATTCATCGAGGGCTTCAGAGC 639

QY 484 ACCAGCTGAGAGTCTGTGTCGCCAGCGCGCAATCGTCCGCCAAGATCGAGTGTGTC 543
Db 640 ACCAGCTGAGAGTCTGTGTCGCCAGCGCGCAATCGTCCGCCAAGATCGAGTGTGTC 699

QY 544 ATTTCCGAGGCCAGCTCATCCAAACAACTCTCGACCCAGGCACTGTCTCTCGAA 603
Db 700 ATTTCCGAGGCCAGCTCATCCAAACAACTCTCGACCCAGGCACTGTCTCTCGAA 759

QY 604 GACAGCAATTCGCGGATACCGTCAAGCCAAATTTTCACGGCCAGCTTCGTCCTCAT 663
Db 760 GACAGCAATTCGCGGATACCGTCAAGCCAAATTTTCACGGCCAGCTTCGTCCTCAT 819

QY 664 CGTCAACGTCGAGAACGACCTGTCCGGTGTGACTCTCAGACACACAGAGTGCCTAC 723
Db 820 CGTCAACGTCGAGAACGACCTGTCCGGTGTGACTCTCAGACACACAGAGTGCCTAC 879

QY 724 CTCATGACATGTCTCTTCGACACCATTCACCCAGCACCGTTCGACACCAAGGTGTC 783
Db 880 CTCATGACATGTCTCTTCGACACCATTCACCCAGCACCGTTCGACACCAAGGTGTC 939

QY 784 CCCTTCTGTGACTGTTTACCCATCAAGATGATCACTAGTCACTCTCCAGTCTCTG 843
Db 940 CCCTTCTGTGACTGTTTACCCATCAAGATGATCACTAGTCACTCTCCAGTCTCTG 999

QY 844 AAAAAATATTACGGCCATGCTGAGTAAACCGCTTCGCGCCGACCCAGGGGGTCCGCTAC 903
Db 1000 AAAAAATATTACGGCCATGCTGAGTAAACCGCTTCGCGCCGACCCAGGGGGTCCGCTAC 1059

QY 904 GCTAAGAGCTCATCGCCGCTGACCCATCGCTGTCCAGATGACACAGTTCGAC 963
Db 1060 GCTAAGAGCTCATCGCCGCTGACCCATCGCTGTCCAGATGACACAGTTCGAC 1119

QY 964 CACACTTTGGACTTCGAGCCCGGCTACCTTTCCGCTCAACTCTCTCTAGCGGACTTT 1023
Db 1120 CACACTTTGGACTTCGAGCCCGGCTACCTTTCCGCTCAACTCTCTCTAGCGGACTTT 1179

QY 1024 TCGCATGACACGGGATCATCTCCATCTCTTTGGTTTAGTCTGTACACAGGCACTAAG 1083

1742	Db	GCTAACGAGCTCATCGCCCGCTGACCCACTCGCCTGTCCAGGATGACACGAGTTTCCAAC	1801
964	Qy	CACACTTTTGACTCGAGCCCGGCTACCTTTCCGCTCAACTCTACTCTCTACGGGACTTT	1023
1802	Db	CACACTTTTGACTCGAGCCCGGCTACCTTTCCGCTCAACTCTACTCTCTACGGGACTTT	1861
1024	Qy	TCGGATGACAAACGGGATCATCTCGATTCTCTTTAGTCTGTGATCAACGGGACTAAG	1083
1862	Db	TCGGATGACAAACGGGATCATCTCCATTCTCTTTAGTCTGTGATCAACGGGACTAAG	1921
1084	Qy	CCGCTATCTACCAAGACCGGTGGAGATATCACCCAGACAGATGGATTCTCGTCTGCTTGG	1143
1922	Db	CCGCTATCTACCAAGACCGGTGGAGATATCACCCAGACAGATGGATTCTCGTCTGCTTGG	1981
1144	Qy	ACGGTTCCGTTTGGTCTCCGCTTTGTACGTCGAGATGATGACGTCAGCGCGGACGAGG	1203
1982	Db	ACGGTTCCGTTTGGTCTCCGCTTTGTACGTCGAGATGATGACGTCAGCGCGGACGAGG	2041
1204	Qy	CCGCTGGTCCGTTCTTTGGTTTAATGATCGCGTTGTCCCGCTGCATCGGTTCCGGTTGAT	1263
2042	Db	CCGCTGGTCCGTTCTTTGGTTTAATGATCGCGTTGTCCCGCTGCATCGGTTCCGGTTGAT	2101
1264	Qy	GCCTTTGGGAGATGTATCCCGGGATAGCTTTGTGAGGGGGTTGAGCTTTGCTAGATCTGGG	1323
2102	Db	GCCTTTGGGAGATGTATCCCGGGATAGCTTTGTGAGGGGGTTGAGCTTTGCTAGATCTGGG	2161
1324	Qy	GGTGATTGGCGGAGTGTTTTGCTTAG	1350
2162	Db	GGTGATTGGCGGAGTGTTTTGCTTAG	2188

RESULT 7	
AAQ11174	
ID	AAQ11174 standard; DNA; 6756 BP.
XX	
XX	
AC	AAQ11174;
XX	
XX	
DT	25-MAR-2003 (revised)
DT	31-MAY-1991 (first entry)
XX	
XX	
DE	Sequence, from overlapping clones, encoding chromosomal phytase.
XX	
XX	
KW	Microbial phytase; animal feeds; inositol; inorganic phosphates; ss.
XX	
OS	Synthetic.

XX	Disclosure; Page 32; 61pp; English.
PS	
XX	
CC	This sequence is a compilation of the respective sequences of clones pAF
CC	2-3, pAF 2-6 and pAF 2-7 identified using oligonucleotide probes. The use
CC	of recombinant DNA methods for the the enzyme prodn. allows the large
CC	scale prodn. of proteins and peptides having phytase activity. These are
CC	used for the conversion of phytate to inositol and inorganic phosphate
CC	and can be used in industrial processes. The phosphate content of manure
CC	thus can be decreased. See also AAQ1157-73 and AAQ11175. (Updated on 25-
CC	MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI
CC	field.)
XX	
SQ	Sequence 6756 BP; 1615 A; 1718 C; 1707 G; 1716 T; 0 U; 0 Other;
	Query Match 99.8%; Score 1347; DB 2; Length 6756;
	Best Local Similarity 100.0%; Pred. No. 0;
	Matches 1347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	4 CTGGCAGTCCC GCCCTCGAGAATCAATCAGTTGCGATACGCTCCGATCAGGGGTATCAA 63
DB	369 CTGGCAGTCCCCGCCCTCGAATAATCAATCAGTTGCGATACGCTCCGATCAGGGGTATCAA 428
QY	64 TGCTTCTCCGAGACTTCGCATCTTTGGGGTCAATACGCACCGTTCTTCTCTCGGCAAAAC 123
DB	429 TGCTTCTCCGAGACTTCGCATCTTTGGGGTCAATACGCACCGTTCTTCTCTCGGCAAAAC 488
QY	124 GAATCGGTGTAATCTCCCGTAGAGTGCCGCGGGATGCAGAGTCACTTTTCGTCAGGTCCCTC 183
DB	489 GAATCGGTGTAATCTCCCGTAGAGTGCCGCGGGATGCAGAGTCACTTTTCGTCAGGTCCCTC 548
QY	184 TCCCGTTCATGGAGCGGGGTATCCGACCGACTCCAGAGGCGAAGAAATACTCCGCTCATTT 243
DB	549 TCCCGTTCATGGAGCGGGGTATCCGACCGACTCCAGAGGCGAAGAAATACTCCGCTCATTT 608
QY	244 GAGGAGATCACGAGAAACGCGACCACTTTTGACGGAATAATATGCTTCTCTGAAGAATAC 303
DB	609 GAGGAGATCACGAGAAACGCGACCACTTTTGACGGAATAATATGCTTCTCTGAAGAATAC 668
QY	304 AACTACAGTTGGGTGCAGATGACCTGACTCCCTTCGGAGAACAGAGCTAGTCAACTCC 363
DB	669 AACTACAGTTGGGTGCAGATGACCTGACTCCCTTCGGAGAACAGAGCTAGTCAACTCC 728
QY	364 GGCAATCAAGTTCTACAGCGGTACGAATCGCTCACAAGGAAACATCGTTCCATTCAATCCA 423
DB	729 GGCAATCAAGTTCTACAGCGGTACGAATCGCTCACAAGGAAACATCGTTCCATTCAATCCA 788
QY	424 TCCTCTGGCTCCAGCCGGTGATCGGCTCGGCAAGAAATTCATCGAGGGCTCCAGAGC 483
DB	789 TCCTCTGGCTCCAGCCGGTGATCGGCTCGGCAAGAAATTCATCGAGGGCTCCAGAGC 848
QY	484 ACCAAGCTGAAGGATCCTCGTGCCAGCCGGGCCAATCGTCCGCCAAGATCCAGCTGGTC 543
DB	849 ACCAAGCTGAAGGATCCTCGTGCCAGCCGGGCCAATCGTCCGCCAAGATCCAGCTGGTC 908
QY	544 ATTTCCGAGCCAGCTCATCCAAACAATCTTCGACCCAGGCACCTGCACTGTCTTCGAA 603
DB	909 ATTTCCGAGCCAGCTCATCCAAACAATCTTCGACCCAGGCACCTGCACTGTCTTCGAA 968
QY	604 GACAGGGAATTGCGCGATACCCTCGGAAGCCAAATTTCCACCGCCACGTTCTGTCCTCCATT 663
DB	969 GACAGGGAATTGCGCGATACCCTCGGAAGCCAAATTTCCACCGCCACGTTCTGTCCTCCATT 1028
QY	664 CGTCAACGTCGTGAGAACGACCTGTCCGGTGTGACTCTCACAGACACAGAAGTGACCTAC 723
DB	1029 CGTCAACGTCGTGAGAACGACCTGTCCGGTGTGACTCTCACAGACACAGAAGTGACCTAC 1088
QY	724 CTCATGGA CATGTGCTCTTCGACACCATCTCCACAGCACCGTCGACACCAAGCTGCTCC 783
DB	1089 CTCATGGA CATGTGCTCTTCGACACCATCTCCACAGCACCGTCGACACCAAGCTGCTCC 1148
QY	784 CCCTTCTGTGACTGTTTACCCTATGACGAATGGATCAACTACGACTACCTCCAGTCTCTTG 843

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Db 1149 CCCTTCCTGTGACCTGTTCAACCATGACGAATGATGAACATACGACTACCTCCAGTCCTTG 1208
Qy 844 AAAAAGTATTACGGCCATGTTGCAAGTAAACCCGCTCGGCCCGACCCAGGGCGTCCGGCTAC 903
Db 1209 AAAAAGTATTACGGCCATGTTGCAAGTAAACCCGCTCGGCCCGACCCAGGGCGTCCGGCTAC 1268
Qy 904 GCTAACGAGCTATCGCCCGCTGACCCACTCGGCTGTCCAGATGACACAGTTCACAC 963
Db 1269 GCTAACGAGCTATCGCCCGCTGACCCACTCGGCTGTCCAGATGACACAGTTCACAC 1328
Qy 964 CACACTTTGGACTCGAGCCCGGCTACCTTTCCGCTCAACTCTACTCTCTACGGGACTTT 1023
Db 1329 CACACTTTGGACTCGAGCCCGGCTACCTTTCCGCTCAACTCTACTCTCTACGGGACTTT 1388
Qy 1024 TCGCATGAACAGGATCAATCCATCTCTCTTTAGTCTGTGTAACAGGCACTAAG 1083
Db 1389 TCGCATGAACAGGATCAATCCATCTCTCTTTAGTCTGTGTAACAGGCACTAAG 1448
Qy 1084 CCGCTATCTACACGACCGTGGAGATATACCCAGACAGATGATCTGCTGCTTGG 1143
Db 1449 CCGCTATCTACACGACCGTGGAGATATACCCAGACAGATGATCTGCTGCTTGG 1508
Qy 1144 ACGTTCGCTTTGCTTCGCGTTTGTAGCTCGAGATGATGACAGTGTCAAGGCGGACGAG 1203
Db 1509 ACGTTCGCTTTGCTTCGCGTTTGTAGCTCGAGATGATGACAGTGTCAAGGCGGACGAG 1568
Qy 1204 CCGTGTGCTCTGCTGTTTAAATGATCGCGTTTCTCCGCTGCATGGGTCTCGTTGAT 1263
Db 1569 CCGTGTGCTCTGCTGTTTAAATGATCGCGTTTCTCCGCTGCATGGGTCTCGTTGAT 1628
Qy 1264 GCTTTGGGGAGATGATACCCGGGATAGCTTTGTAGGGGGTTGAGCTTTGTAGATCTGGG 1323
Db 1629 GCTTTGGGGAGATGATACCCGGGATAGCTTTGTAGGGGGTTGAGCTTTGTAGATCTGGG 1688
Qy 1324 GGTGATTGGGGAGTGTGTTGCTTAG 1350
Db 1689 GGTGATTGGGGAGTGTGTTGCTTAG 1715

RESULT 8
AAAT65137
ID AAAT65137 standard; cDNA; 6756 BP.
XX
AC AAAT65137;
XX
DT 17-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 21-AUG-1997 (first entry)
XX
DE Aspergillus ficuum phytase genomic DNA.
XX
KW Phytase; phytate; inositol; animal feed; ss.
XX
OS Aspergillus ficuum; NRRL 3135.
XX
FH Key Location/Qualifiers
FT primer_bind /*tag= d complement(210..231)
FT /*note= "oligonucleotide 1"
FT exon 211..253
FT /*tag= a
FT intron 254..355
FT /*tag= b
FT exon 356..1715
FT /*tag= c complement(845..865)
FT primer_bind /*tag= f
FT /*note= "oligonucleotide 3"
FT primer_bind 1109..1129
FT /*tag= e
FT /*note= "oligonucleotide 2"
FT primer_bind 1867..1890
FT /*tag= g
```

```
FT /note= "oligonucleotide 4"
XX EP779037-A1.
XX 18-JUN-1997.
XX
XX 27-SEP-1990; 96EP-00202943.
XX
XX 27-SEP-1989; 89EP-00202436.
XX 17-AUG-1990; 90EP-00202231.
XX 27-SEP-1990; 90EP-00202565.
XX
XX (KONN ) GIST-BROCADES NV.
XX (STAM ) DSM NV.
XX
XX Van Paridon RM, Veenstra AE, Luiten RGM, Seltens GCM;
XX Van Gorcom RF, Van Hartingsveldt W;
XX
XX WPI; 1997-312513/29.
XX P-PSDB; AAW15124.
XX
XX Fungal phytase - releases inorganic phosphate from myoinositol phosphate,
XX useful to prepare animal feed and reduce phytate levels in manure.
XX
XX Example 8; Fig 6; 61pp; English.
XX
XX Genomic DNA (AAAT65137) comprises the phytase gene locus of Aspergillus
XX ficum and includes a coding sequence, interrupted by a single intron,
XX for the 467-amino acid enzyme (AAW15124). The DNA sequence was deduced
XX from clones pAF 2-3, pAF 2-6 and pAF 2-7, which were identified in
XX genomic DNA using probes (see also AAT65138-40) based on CNBr peptides
XX (AAW15128-29) of the phytase. PCR primers (AAT65144-47) based on gene
XX sequences were used to amplify a full-length cDNA clone (AAT65136) for
XX the phytase. Characterisation of the phytase gene will allow large-scale
XX prodn. of phytase in transformed host cells for use e.g. in the food and
XX animal feed industries, and for reducing phytate levels in manure.
XX (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to
XX correct PR field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated
XX on 25-MAR-2003 to correct PI field.) (Updated on 17-OCT-2003 to
XX standardise OS field)
XX
SQ Sequence 6756 BP; 1615 A; 1714 C; 1712 G; 1715 T; 0 U; 0 Other;
Query Match 99.8%; Score 1347; DB 2; Length 6756;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 CTGGCAGTCCCGCTCGAGAAATCAATCCAGTTCGATACGGTCGATCAGGGGTATCAA 63
Db 369 CTGGCAGTCCCGCTCGAGAAATCAATCCAGTTCGATACGGTCGATCAGGGGTATCAA 428
Qy 64 TGCTTCTCCGAGACTTCGATCTTTGGGGTCAATACGACCGTTCCTCTCTGCGCAAC 123
Db 429 TGCTTCTCCGAGACTTCGATCTTTGGGGTCAATACGACCGTTCCTCTCTGCGCAAC 488
Qy 124 GAATCGGTTCATCTCCCTGAGTGCCTCCGATCGAGATCAGATCAGTTCGCTCAGTCCTC 183
Db 489 GAATCGGTTCATCTCCCTGAGTGCCTCCGATCGAGATCAGATCAGTTCGCTCAGTCCTC 548
Qy 184 TCCCGTCATGGAGCGCGGTATCCGACCGACTCCAGGCGGCAAGATATCTCGCTCTCAT 243
Db 549 TCCCGTCATGGAGCGCGGTATCCGACCGACTCCAGGCGGCAAGATATCTCGCTCTCAT 608
Qy 244 GAGGAGATCCAGCAGACGCGACCACTTTGACGGGAAATATGCTTCCTGAAGACATAC 303
Db 609 GAGGAGATCCAGCAGACGCGACCACTTTGACGGGAAATATGCTTCCTGAAGACATAC 668
Qy 304 AACTACAGTTGGGTGCGAGATGACTGCTCCCTCCGAGAACAGGAGCTAGTCAACTCC 363
Db 669 AACTACAGTTGGGTGCGAGATGACTGCTCCCTCCGAGAACAGGAGCTAGTCAACTCC 728
Qy 364 GGCATCAAGTTCTTACCAGCGGTACCAATCGCTCAACAGGACATCGTTCCATTCATCCGA 423
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Db 729 GGATCAAGATTCTACAGCGGTACGAATCGTCTCAAGAGAACATCGTTTCCATTCATCCGA 788
Qy 424 TCCTCTGCTCAGCGCGGTGATCGCTCCGCGCAAGAAATTCATCGAGGGGTCCAGAGC 483
Db 789 TCCTCTGCTCAGCGCGGTGATCGCTCCGCGCAAGAAATTCATCGAGGGGTCCAGAGC 848
Qy 484 ACCAAGCTGAAGATTCCTGCTGCGCAGCGCGCAATGCTGCGCCCAAGATCGAGTGGTC 543
Db 849 ACCAAGCTGAAGATTCCTGCTGCGCAGCGCGCAATGCTGCGCCCAAGATCGAGTGGTC 908
Qy 544 ATTTCCGAGGCGAGCTCATCAACAACACTCTCGACCCAGGCACTGCATCTGCTTCCAA 603
Db 909 ATTTCCGAGGCGAGCTCATCAACAACACTCTCGACCCAGGCACTGCATCTGCTTCCAA 968
Qy 604 GACAGCGAATTGGCGGATACCGTTCGAGCCAAATTCACCGCCACGTTGCTCCCTCCATT 663
Db 969 GACAGCGAATTGGCGGATACCGTTCGAGCCAAATTCACCGCCACGTTGCTCCCTCCATT 1028
Qy 664 CGTCAACCTCTGGAGACGACTGTCGCGTGTGACTCTCAAGACACAGAGTACCTAC 723
Db 1029 CGTCAACCTCTGGAGACGACTGTCGCGTGTGACTCTCAAGACACAGAGTACCTAC 1088
Qy 724 CTCATGACATGTGCTCTCTCGACACCATCTCCACGACCGTTCGACACCAAGCTGCC 783
Db 1089 CTCATGACATGTGCTCTCTCGACACCATCTCCACGACCGTTCGACACCAAGCTGCC 1148
Qy 784 CCCTTCTGTGACTGTTCAACCATGACGAATGGATCACTACGACTACCTCCAGTCTTG 843
Db 1149 CCCTTCTGTGACTGTTCAACCATGACGAATGGATCACTACGACTACCTCCAGTCTTG 1208
Qy 844 AAAAGATATTACGGCCATGTGTCAGGTAACCCGGTCCGCGCCGACCCAGGGGTCCGGTAC 903
Db 1209 AAAAGATATTACGGCCATGTGTCAGGTAACCCGGTCCGCGCCGACCCAGGGGTCCGGTAC 1268
Qy 904 GCTAACGAGCTCATCGCCGCTGTGACCCACTCGCTGTCACGATGACACAGTTCACAC 963
Db 1269 GCTAACGAGCTCATCGCCGCTGTGACCCACTCGCTGTCACGATGACACAGTTCACAC 1328
Qy 964 CACACTTTGGACTGAGCCCGGCTACCTTTCCGCTCAACTCTCTCTACGCGACTTT 1023
Db 1329 CACACTTTGGACTGAGCCCGGCTACCTTTCCGCTCAACTCTCTCTACGCGACTTT 1388
Qy 1024 TCGCATGACACGGCATCATCTCCATCTCTTTGCTTTAGTGTGTACACGCACTAAG 1083
Db 1389 TCGCATGACACGGCATCATCTCCATCTCTTTGCTTTAGTGTGTGTACACGCACTAAG 1448
Qy 1084 CGGCTATCTACACGACCGTGGAGATATCAACGACAGATGATCTCTCTGCTTGG 1143
Db 1449 CGGCTATCTACACGACCGTGGAGATATCAACGACAGATGATCTCTCTGCTTGG 1508
Qy 1144 ACGGTTCCGTTTGGCTTCGCTTTGACGTCGAGATGATGACGAGTGTACGCGGACGAG 1203
Db 1509 ACGGTTCCGTTTGGCTTCGCTTTGACGTCGAGATGATGACGAGTGTACGCGGACGAG 1568
Qy 1204 CCGCTGCTCGTGTCTTGGTTAATGATCGGTTGTCGCGCTGCATGGTGTCCGGTTGAT 1263
Db 1569 CCGCTGCTCGTGTCTTGGTTAATGATCGGTTGTCGCGCTGCATGGTGTCCGGTTGAT 1628
Qy 1264 GCTTTGGGAGATGATACCCGGGATAGCTTTGTAGAGGGGTTGAGCTTTGCTAGATCTGG 1323
Db 1629 GCTTTGGGAGATGATACCCGGGATAGCTTTGTAGAGGGGTTGAGCTTTGCTAGATCTGG 1688
Qy 1324 GGTGATTTGGGCGAGTGTGTTGCTTAG 1350
Db 1689 GGTGATTTGGGCGAGTGTGTTGCTTAG 1715

RESULT 9

ABX13436

ID ABX13436 standard; DNA; 6756 BP.

XX

AC

ABX13436;

XX

DT 04-JUN-2003 (first entry)
XX Plasmids pAF2-3, pAF2-6, pAF2-7 phytase corresponding to Genbank A19451.
XX
XX Expression cassette; transgenic; promoter; LOX5; plant; food production;
XX animal feed; seed; stress resistance; disease resistance; starch content;
XX lipid content; dormancy; fibre content; pharmaceutical production;
XX fine chemical production; sterile plant; vitamin; flavouring; perfume;
XX dye; cotyledon; embryonic tissue; stress factor; LOX; ds.
OS Arabidopsis thaliana.
OS Synthetic.
PN DE10127882-A1.
XX
XX 12-DEC-2002.
XX
XX 11-JUN-2001; 2001DE-01027882.
XX
XX 11-JUN-2001; 2001DE-01027882.
XX
XX (BADI) BASF PLANT SCI GMBH.
PA
XX Bischoff F, Feussner I, Loyall LP;
PI
XX WPI; 2003-279966/28.
XX
XX Cassette for expressing transgene, useful e.g. in production of
PT pharmaceuticals and fine chemicals, contains promoter from the LOX5 gene
PT of Arabidopsis, provides cotyledon-specific expression.
XX
XX Claim 5; Page: 28pp; German.
XX
XX This invention describes a novel cassette for the transgenic expression
CC of nucleic acid containing the promoter of the LOX5 gene from Arabidopsis
CC thaliana or deletion variants of the LOX5 promoter which are functionally
CC linked to the nucleic acid of the invention. The cassette is used to
CC prepare transgenic organisms, especially plants, for production of foods,
CC animal feeds, seeds (including those with increased resistance to stress
CC and disease, altered starch/lipid contents or dormancy, or altered fibre
CC content), pharmaceuticals (especially antibodies, vaccines, enzymes and
CC pharmaceutical proteins) and fine chemicals (especially enzymes,
CC vitamins, amino acids, sugars, (un)saturated fatty acids, flavourings,
CC perfumes and dyes), also to produce sterile plants. The LOX5 promoter,
CC provides strong and specific expression in cotyledons and/or other early
CC embryonic tissue, so can degrade, or protect against, stress factors to
CC which these tissues are particularly sensitive. Since cotyledons are the
CC main storage organs of seeds, expressing transgenes in them produces
CC targeted increases/modifications in nutritional value. Expression in the
CC cotyledons is homogeneous, there are no side effects on other plant
CC organs (pollen) and the promoter is functional in a wide variety of
CC plants (ornamentals or crops). This sequence represents a nucleic acid
CC sequence associated with the Arabidopsis thaliana LOX gene described in
CC the disclosure of the invention
XX
XX Sequence 6756 BP; 1615 A; 1712 C; 1712 G; 1714 T; 0 U; 3 Other;
Qy
Query Match 99.8%; Score 1347; DB 8; Length 6756;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 CTGGCAGTCCCGCTCGAGAAATCAATCCAGTTGCGATACCGTTCGATCAGGGGTATCAA 63
Db 369 CTGGCAGTCCCGCTCGAGAAATCAATCCAGTTGCGATACCGTTCGATCAGGGGTATCAA 428
Qy 64 TGCTTCTCCGAGACTTCGCATCTTTGGGGTCAATACGACCGCTTCTTCTCTGCGCAAC 123
Db 429 TGCTTCTCCGAGACTTCGCATCTTTGGGGTCAATACGACCGCTTCTTCTCTGCGCAAC 488
Qy 124 GAATCGGTATCTCCCTGAGGTGCCCGGATGCGAGTGCAGTTCGCTCAGTCTCTC 183
Db 489 GAATCGGTATCTCCCTGAGGTGCCCGGATGCGAGTGCAGTTCGCTCAGTCTCTC 548

184 TCCCGTCATGAGCGGGTATCCGACCGACTCCAAAGGCAAGAAATACCTCCGCTCTCAT 243
549 TCCCGTCATGAGCGGGTATCCGACCGACTCCAAAGGCAAGAAATACCTCCGCTCTCAT 608
244 GAGGAGATCCAGCAGAACCGGACCACTTTGACGGAATAATGCCCTCTCTGAAGACATAC 303
609 GAGGAGATCCAGCAGAACCGGACCACTTTGACGGAATAATGCCCTCTCTGAAGACATAC 668
304 AACTACAGCTTGGGTGACAGATGACCTGACTCCCTTCGGAGAACAGGAGTAGTCAACTCC 363
669 AACTACAGCTTGGGTGACAGATGACCTGACTCCCTTCGGAGAACAGGAGTAGTCAACTCC 728
364 GGATCAAGTTTACAGCGGTAACGAAATGCTCACAAGGAAATATGCTTCACTTCATCCGA 423
729 GGATCAAGTTTACAGCGGTAACGAAATGCTCACAAGGAAATATGCTTCACTTCATCCGA 788
424 TCCCTGGCTCCAGCGCGGTGCTCGCTCCGGAAGAAATTCATCGAGGCTTCCAGAGC 483
789 TCCCTGGCTCCAGCGCGGTGCTCGCTCCGGAAGAAATTCATCGAGGCTTCCAGAGC 848
484 ACCAAGCTGAAGATCCTCGTCCGCAAGCCGCGCAATTCGTCGCCAAGATCGACGTGGTC 543
849 ACCAAGCTGAAGATCCTCGTCCGCAAGCCGCGCAATTCGTCGCCAAGATCGACGTGGTC 908
544 ATTTCCGAGCGAGCTCATCCAAACACACTCTCGACCGGACCTGCACTGCTTCGAA 603
909 ATTTCCGAGCGAGCTCATCCAAACACACTCTCGACCGGACCTGCACTGCTTCGAA 968
604 GACAGCAATTTGGCCGATACCGTCGAAGCCAAATTCACCGCCACGTTTCGTCCTCCATT 663
969 GACAGCAATTTGGCCGATACCGTCGAAGCCAAATTCACCGCCACGTTTCGTCCTCCATT 1028
664 CGTCAACGCTGGAGAACGACCTGTCGGGTGACCTCTCACAGACACAGAGTGAAGTAC 723
1029 CGTCAACGCTGGAGAACGACCTGTCGGGTGACCTCTCACAGACACAGAGTGAAGTAC 1088
724 CTGATGACATGCTCTCTTCGACACCATCTCCACAGCACCTGTCGACACCAAGCTGTC 783
1089 CTGATGACATGCTCTCTTCGACACCATCTCCACAGCACCTGTCGACACCAAGCTGTC 1148
784 CCCTTCTGTGACCTGTTCAACCATGACGAATGATCACTACGACTACCTCCAGTCTTG 843
1149 CCCTTCTGTGACCTGTTCAACCATGACGAATGATCACTACGACTACCTCCAGTCTTG 1208
844 AAAAGTATTACGGCCATGTCGAGTAACCGCTCGGCGCCGACCCAGGCGCTCGGCTAC 903
1209 AAAAGTATTACGGCCATGTCGAGTAACCGCTCGGCGCCGACCCAGGCGCTCGGCTAC 1268
904 GCTAACGAGCTCATCGCCGCTCTGACCACTCGCTTCCACGATGACACAGTTCACAC 963
1269 GCTAACGAGCTCATCGCCGCTCTGACCACTCGCTTCCACGATGACACAGTTCACAC 1328
964 CACATTTGGACTCGAGCCGGCTACCTTTCCGCTCAACTCTACTCTCTACGCGGACTTT 1023
1329 CACATTTGGACTCGAGCCGGCTACCTTTCCGCTCAACTCTACTCTCTACGCGGACTTT 1388
1024 TCGATGACACAGGCTCATCTCCATCTCTTTCTTTAGTCTGTGTAACGCGCACTAAG 1083
1389 TCGATGACACAGGCTCATCTCCATCTCTTTCTTTAGTCTGTGTAACGCGCACTAAG 1448
1084 CCGTATCTACACAGCGTGGAGAAATATACCCAGACAGATGATCTCGTCTGCTTGG 1143
1449 CCGTATCTACACAGCGTGGAGAAATATACCCAGACAGATGATCTCGTCTGCTTGG 1508
1144 ACGGTTCCGTTGCTTCCGCTTCTGACGTGAGATGATGAGTCTGAGGCGGAGCAGGAG 1203
1509 ACGGTTCCGTTGCTTCCGCTTCTGACGTGAGATGATGAGTCTGAGGCGGAGCAGGAG 1568
1204 CCGTGTGCTCGTGTCTTGGTTAATGATCGCGTGTTCGCGTGCATGAGGTGCGGTTGAT 1263
1569 CCGTGTGCTCGTGTCTTGGTTAATGATCGCGTGTTCGCGTGCATGAGGTGCGGTTGAT 1628
1264 GCTTTGGGAGATGATACCCGGGATAGCTTTGTGAGGGGGTTGAGCTTGTAGATCTGGG 1323

Db 1629 GCTTTGGGAGATGATACCCGGATAGCTTTGTGAGGGGTTGAGCTTGTCTAGATCTGGG 1688
Qy 1324 GGTGATTGGCGGAGTGTTTTGCTTAG 1350
Db 1689 GGTGATTGGCGGAGTGTTTTGCTTAG 1715
RESULT 10
AAT65136
ID AAT65136 standard; cDNA; 1404 BP.
XX
AC AAT65136;
XX
DT 17-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 21-AUG-1997 (first entry)
XX
DE Aspergillus ficuum phytase cDNA.
XX
KW Phytase; phytate; inositol; animal feed; ss.
XX
OS Aspergillus ficuum; NRRL 3135.
XX
FH Key Location/Qualifiers
FT sig_peptide 1..69
FT mat_peptide 70..1401
FT /tag= a
FT /tag= b
XX
PN EP779037-A1.
XX
PD 18-JUN-1997.
PF 27-SEP-1990; 95EP-00202943.
PR 27-SEP-1989; 89EP-00202436.
PR 17-AUG-1990; 90EP-00202231.
PR 27-SEP-1990; 90EP-00202565.
XX
PA (KONN) GIST-BROCADES NV.
PA (STAM) DSM NV.
PI Van Paridon PA, Veenstra AE, Luiten RGM, Seiten GCM;
PI Van Gorcom RFM, Van Hartingsveldt W;
XX
DR WPI; 1997-312513/29.
DR P-FSDB; AAW15124.
XX
PT Fungal phytase - releases inorganic phosphate from myoinositol phosphate,
PT useful to prepare animal feed and reduce phytate levels in manure.
XX
PS Claim 1; Fig 8; 61pp; English.
XX
CC A cDNA clone (AAT65136) codes for Aspergillus ficuum phytase (AAW15124),
CC an enzyme that catalyses the conversion of phytate to inositol and
CC inorganic phosphate. It was obtd. by PCR amplification of A. ficuum
CC mRNA/cDNA hybrids using primers (see also AAT65144-47) based on a genomic
CC phytase sequence (see also AAT65137). Isolation of this cDNA clone allows
CC large-scale prodn. of recombinant phytase in transformed host cells for
CC use e.g. in the food and animal feed industries, and for reducing phytate
CC levels in animal manure. (Updated on 25-MAR-2003 to correct PR field.)
CC (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to
CC correct PA field.) (Updated on 25-MAR-2003 to correct PI field.) (Updated
CC on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 1404 BP; 293 A; 437 C; 343 G; 331 T; 0 U; 0 Other;

Query Match 99.7%; Score 1345.4; DB 2; Length 1404;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1346; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 4 CTGGCAGTCCCGCCCTCGAGAAATCAATCCAGTTGCGATACGGTTCGATCAGGGGTATCAA 63

Db 58 CTGGCAGTCCCGCTCGAAGAAATCAATCCAGTTCGGATACGGTCGATCAGGGGTATCAA 117
QY 64 TCTTTCTCGAGACTTCGATCTTTGGGGTCAATAACGACCGGTTCCTCTCTCGGCAAC 123
Db 118 TCGTTCTCGAGACTTCGATCTTTGGGGTCAATAACGACCGGTTCCTCTCTCGGCAAC 177
QY 124 GAATCGGTCAATCTCCCTGAGGTGCGCGCGGATGACAGATCACTTTGCTCAGGTCTC 183
Db 178 GAATCGGTCAATCTCCCTGAGGTGCGCGCGGATGACAGATCACTTTGCTCAGGTCTC 237
QY 184 TCCCGTCAATGAGCGGTATCCGACCGACTCCAGGGCAAGAAATACTCCGCTCTCAT 243
Db 238 TCCCGTCAATGAGCGGTATCCGACCGACTCCAGGGCAAGAAATACTCCGCTCTCAT 297
QY 244 GAGGAGATCCAGCAACCGGACCACTTTGACGGAATAATGCTTCCGGAAGACATAC 303
Db 298 GAGGAGATCCAGCAACCGGACCACTTTGACGGAATAATGCTTCCGGAAGACATAC 357
QY 304 AACTACAGCTGGGTGACAGATGACCTGACTCCCTTCGAGAAACAGGAGTAGTCAACTCC 363
Db 358 AACTACAGCTGGGTGACAGATGACCTGACTCCCTTCGAGAAACAGGAGTAGTCAACTCC 417
QY 364 GGCATCAAGTTCTACAGCGGTACGAATCGCTCAAAAGGAACATCGTTCATTCATCCGA 423
Db 418 GGCATCAAGTTCTACAGCGGTACGAATCGCTCAAAAGGAACATCGTTCATTCATCCGA 477
QY 424 TCCCTGCTCCAGCGGTGATCGCTCCGCGAAGAAATTCATCGAGGGCTTCCAGAGC 483
Db 478 TCCCTGCTCCAGCGGTGATCGCTCCGCGAAGAAATTCATCGAGGGCTTCCAGAGC 537
QY 484 ACCAAGCTGAAGAGTCTCGTSCCAGCCGCGCAATCGTCCGCAAGATCGAGCTGGTC 543
Db 538 ACCAAGCTGAAGAGTCTCGTSCCAGCCGCGCAATCGTCCGCAAGATCGAGCTGGTC 597
QY 544 ATTTCCGAGGCGAGTCAATCAACAACTCTCGACCCAGGACCTGCTGCTTCGAA 603
Db 598 ATTTCCGAGGCGAGTCAATCAACAACTCTCGACCCAGGACCTGCTGCTTCGAA 657
QY 604 GACAGCGAATTTGGCGGTACCGTCCGAGCAATTTACCCGCAAGTTCGCTCCCTCCATT 663
Db 658 GACAGCGAATTTGGCGGTACCGTCCGAGCAATTTACCCGCAAGTTCGCTCCCTCCATT 717
QY 664 CGTCAAGCTGAGAGACGACTCTCGGTGTGACTCTCAAGACAGAAAGTGAAGTAC 723
Db 718 CGTCAAGCTGAGAGACGACTCTCGGTGTGACTCTCAAGACAGAAAGTGAAGTAC 777
QY 724 CTCATGACATGTCTCTTCGACACCATCTCCACAGACCGGTGACACCAAGCTGTCC 783
Db 778 CTCATGACATGTCTCTTCGACACCATCTCCACAGACCGGTGACACCAAGCTGTCC 837
QY 784 CCCTTCTGTGACCTGTTTACCCATGACGAATGATCACTACGACTACCTCCAGTCTTG 843
Db 838 CCCTTCTGTGACCTGTTTACCCATGACGAATGATCACTACGACTACCTCCAGTCTTG 897
QY 844 AAAAAGTATTACGCCATGTGAGGTAAACCGCTGGCCCGACCCAGGCGTCCGCTAC 903
Db 898 AAAAAGTATTACGCCATGTGAGGTAAACCGCTGGCCCGACCCAGGCGTCCGCTAC 957
QY 904 GCTAACGAGTCTATCGCCCGTCTGACCCACTCGCTGTCACGATGACACCAAGTCCAAAC 963
Db 958 GCTAACGAGTCTATCGCCCGTCTGACCCACTCGCTGTCACGATGACACCAAGTCCAAAC 1017
QY 964 CACATTTGACATCGAGCCCGGTACCTTTCCGCTCAACTCTACTCTACGCGGACTTT 1023
Db 1018 CACATTTGACATCGAGCCCGGTACCTTTCCGCTCAACTCTACTCTACGCGGACTTT 1077
QY 1024 TCGCATGACAAACGGCATCATCTCATTTCTTTAGTGTGTGACAAACGCACTAAG 1083
Db 1078 TCGCATGACAAACGGCATCATCTCATTTCTTTAGTGTGTGACAAACGCACTAAG 1137
QY 1084 CCGCTATCTACAGGACCGGTGGAGATATACCCAGACAGATGAGTCTCGTCTGTTGG 1143

Db 1138 CCCTATCTATCAACGACCGTGGAGATATCAACCCAGACAGATGGATTTCTGTCTCTGG 1197
QY 1144 ACGTTTCCGTTTCTCGGTTCGTACGTCGAGATGATGACAGTGTACGCGGAGCAGGAG 1203
Db 1198 ACGTTTCCGTTTCTCGGTTCGTACGTCGAGATGATGACAGTGTACGCGGAGCAGGAG 1257
QY 1204 CCGTGGTCCGTTCTTGGTTAATGATCCGTTGTCCCGTGCATGCGGTTCAT 1263
Db 1258 CCGTGGTCCGTTCTTGGTTAATGATCCGTTGTCCCGTGCATGCGGTTCAT 1317
QY 1264 GCTTTGGGAGATGTACCCGGGATAGCTTTGTGAGGGGTTGAGCTTTGCTAGATCTGG 1323
Db 1318 GCTTTGGGAGATGTACCCGGGATAGCTTTGTGAGGGGTTGAGCTTTGCTAGATCTGG 1377
QY 1324 GGTGATTTGGCGGAGTGTCTTTGCTTAG 1350
Db 1378 GGTGATTTGGCGGAGTGTCTTTGCTTAG 1404

RESULT 11

ADL91263
ID ADL91263 standard; DNA; 2665 BP.
XX
AC ADL91263;
XX AC
DT 17-JUN-2004 (first entry)
XX
DE Mutant phytase, E228K, coding sequence, SEQ ID 23.
XX
KW Mutant; mutein; phytase; enzyme; foodstuff; animal feed;
KW inositol phosphate; gene; ds.
XX
OS Aspergillus niger.
OS Synthetic.
XX
PN WO2004024895-A2.
XX
PD 25-MAR-2004.
XX
PF 15-SEP-2003; 2003WO-US028923.
XX
PR 13-SEP-2002; 2002US-0410736P.
XX
PA (CORR) CORNELL RES FOUND INC.
PA (USDA) US SEC OF AGRIC.
XX
PI Lei X, Mullaney EJ, Ullah AHJ;
XX
DR WPI: 2004-270029/25.
XX P-PSDB; ADL91264.

Novel isolated mutant phytase e.g. PhytA useful for feeding monogastric animals, improving nutritional value of foodstuffs consumed by animal, in vitro hydrolysis of phytate or improving nutritional value of foodstuffs consumed by humans.

Claim 5; SEQ ID NO 23; 215pp; English.

The present invention relates to mutant phytases (I) and their coding sequences (ADL91245-ADL91252, ADL91255-ADL91296, ADL91308 and ADL91309). (I) have altered pH profiles and altered pH optima compared to a corresponding non-mutant phytase. (I) are useful for improving the nutritional value of a foodstuff which involves providing a foodstuff comprising myo-inositol hexakisphosphate, providing (I) and feeding to the animal the foodstuff in combination with (I) under conditions effective to increase the bioavailability of phosphate from phytate. (I) are also useful for feeding a monogastric animal (e.g., fowl species, porcine species, aquatic species, domestic animal chosen from canine species and a feline species, or mammalian species chosen from Oryctolagus, Capra, a Bos, Equus and Ovis species) which involves feeding foodstuff in combination with (I), to the animal. (I) are also useful for producing specific inositol phosphate metabolites or products for nutritional and biomedical applications. The present sequence is the

CC the animal the foodstuff in combination with (I) under conditions
 CC effective to increase the bioavailability of phosphate from phytate. (I)
 CC are also useful for feeding a monogastric animal (e.g., fowl species,
 CC porcine species, aquatic species, domestic animal chosen from canine
 CC species and a feline species, or mammalian species chosen from
 CC Oryctolagus, Capra, a Bos, Equus and Ovis species) which involves feeding
 CC foodstuff in combination with (I) to the animal. (I) are also useful for
 CC producing specific inositol phosphate metabolites or products for
 CC nutritional and biomedical applications. The present sequence is the
 CC coding sequence for one such mutant phytase.
 XX
 SQ

Sequence 2665 BP; 632 A; 808 C; 575 G; 650 T; 0 U; 0 Other;

Query Match 99.7%; Score 1345.4; DB 12; Length 2665;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1346; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CTGGCAGTCCCGCTCGAGAAATCAATCCAGTTGCGATACGGTCCGATCAGGGGTATCAA 63
 DB 842 CTGGCAGTCCCGCTCGAGAAATCAATCCAGTTGCGATACGGTCCGATCAGGGGTATCAA 901
 QY 64 TGCTTCTCCGAGACTTCGCATCTTTGGGTCAATACGACCGTTCTCTCTCTGGGAAAC 123
 DB 902 TGCTTCTCCGAGACTTCGCATCTTTGGGTCAATACGACCGTTCTCTCTCTGGGAAAC 961
 QY 124 GAATCGGTCACTCTCCCTGAGGTGCGCCGCGATGCGAGTCACTTTTCGCTCAGGTCTCTC 183
 DB 962 GAATCGGTCACTCTCCCTGAGGTGCGCCGCGATGCGAGTCACTTTTCGCTCAGGTCTCTC 1021
 QY 184 TCCGCTCATGAGCGCGGTATCCGACCGATCTCCAAAGGCGAAGAAATCTCCGCTCTCAT 243
 DB 1022 TCCGCTCATGAGCGCGGTATCCGACCGATCTCCAAAGGCGAAGAAATCTCCGCTCTCAT 1081
 QY 244 GAGGAGATCCAGCAGACGCGACCACTTTGACGGGAAATATGCTTCCTGAGAGACATAC 303
 DB 1082 GAGGAGATCCAGCAGACGCGACCACTTTGACGGGAAATATGCTTCCTGAGAGACATAC 1141
 QY 304 AACTACAGTTGGTGGATGAGTCACTCTCCCTTCGAGGAGAACAGGAGTGTCAACTCC 363
 DB 1142 AACTACAGTTGGTGGATGAGTCACTCTCCCTTCGAGGAGAACAGGAGTGTCAACTCC 1201
 QY 364 GGCATCAAGTTCTACAGCGGTACGATCGCTACAGAGGACATCTGTCATTCATCCGA 423
 DB 1202 GGCATCAAGTTCTACAGCGGTACGATCGCTACAGAGGACATCTGTCATTCATCCGA 1261
 QY 424 TCCTCTGGCTCCAGCGCGTATCGCTCCGCGCAAGAAATTCATCGAGGGCTTCCAGAGC 483
 DB 1262 TCCTCTGGCTCCAGCGCGTATCGCTCCGCGCAAGAAATTCATCGAGGGCTTCCAGAGC 1321
 QY 484 ACCAAGCTGAGGATCTCTGTCGCCAGCCGCGCAATCTGTCGCCGAGATCGACGTGGTC 543
 DB 1322 ACCAAGCTGAGGATCTCTGTCGCCAGCCGCGCAATCTGTCGCCGAGATCGACGTGGTC 1381
 QY 544 ATTTCCGAGGCGAGCTCATCAACCACTCTCGACCCAGGACCTGCACTGCTTCGAA 603
 DB 1382 ATTTCCGAGGCGAGCTCATCAACCACTCTCGACCCAGGACCTGCACTGCTTCGAA 1441
 QY 604 GACAGCGAATTTGGCCGATACCGTGGAGGCAATTTTCAACGCCCAAGTTCGTCCTCCATT 663
 DB 1442 GACAGCGAATTTGGCCGATACCGTGGAGGCAATTTTCAACGCCCAAGTTCGTCCTCCATT 1501
 QY 664 CGTCAACGCTGAGAGACGACCTGTCGGGTGTCACCTCTACAGACACAGAGTGACCTAC 723
 DB 1502 CGTCAACGCTGAGAGACGACCTGTCGGGTGTCACCTCTACAGACACAGAGTGACCTAC 1561
 QY 724 CTATGAGCATGTGCTCTTTCGACACCATCTCCAGGACCGTTCGACCAAGCTGTCC 783
 DB 1562 CTATGAGCATGTGCTCTTTCGACACCATCTCCAGGACCGTTCGACCAAGCTGTCC 1621
 QY 784 CCCTTCTGACCTGTTTACCCATGACGATGATCACTACGACTACCTCCAGTCCCTG 843
 DB 1622 CCCTTCTGACCTGTTTACCCATGACGATGATCACTACGACTACCTCCAGTCCCTG 1681

QY 844 AAAAGTATTACGGCCATCGTGCAGGTAAACCCGCTCGGCCGACCCAGGGCGTCCGCTAC 903
 DB 1682 AGAAAGTATTACGGCCATCGTGCAGGTAAACCCGCTCGGCCGACCCAGGGCGTCCGCTAC 1741
 QY 904 GCTAACGAGCTCATCGCCGCTCTGACCCACTCGCTGTCACGATGACACAGTTCACAC 963
 DB 1742 GCTAACGAGCTCATCGCCGCTCTGACCCACTCGCTGTCACGATGACACAGTTCACAC 1801
 QY 964 CACACTTTGGACTCGAGCCCGGCTACCTTTTCGCTCAACTCTACTCTCTACCGGACTTT 1023
 DB 1802 CACACTTTGGACTCGAGCCCGGCTACCTTTTCGCTCAACTCTACTCTCTACCGGACTTT 1861
 QY 1024 TCGCATGACAAAGGATCATCTCCATCTCTTTAGTCTCTACAAAGGACTAAG 1083
 DB 1862 TCGCATGACAAAGGATCATCTCCATCTCTTTAGTCTCTACAAAGGACTAAG 1921
 QY 1084 CCGCTATCTACCAAGACCGTGGAGAAATATACCCAGACAGATGGATCTCGTCTGCTTGG 1143
 DB 1922 CCGCTATCTACCAAGACCGTGGAGAAATATACCCAGACAGATGGATCTCGTCTGCTTGG 1981
 QY 1144 AGGTTCCGTTTCTGCTTCGCTTGTGACGTGAGATGTCAGTGTGACGGGAGCAGAG 1203
 DB 1982 ACGGTTCCGTTTCTGCTTCGCTTGTGACGTGAGATGTCAGTGTGACGGGAGCAGAG 2041
 QY 1204 CCGCTGGTCCGCTGCTTGGTTAATGATCGGTTGTCCGCTGTCATGGGTGTCGGTTGAT 1263
 DB 2042 CCGCTGGTCCGCTGCTTGGTTAATGATCGGTTGTCCGCTGTCATGGGTGTCGGTTGAT 2101
 QY 1264 GCTTTGGGAGATGATACCCGGGATAGCTTTGTGAGGGGTTGAGCTTTGCTAGATCTGGG 1323
 DB 2102 GCTTTGGGAGATGATACCCGGGATAGCTTTGTGAGGGGTTGAGCTTTGCTAGATCTGGG 2161
 QY 1324 GTGTGATGGCGGAGTGTGTTTGTCTTAG 1350
 DB 2162 GTGTGATGGCGGAGTGTGTTTGTCTTAG 2188

RESULT 13

ADL91247

ID ADL91247 standard; DNA; 2665 BP.

AC ADL91247;

XX

DT 17-JUN-2004 (first entry)

XX

DE Mutant phytase, K300B, coding sequence, SEQ ID 7.

XX

KW Mutant; mutein; phytase; enzyme; foodstuff; animal feed;

XX

KW inositol phosphate; gene; ds.

XX

OS Aspergillus niger.

XX

OS Synthetic.

XX

PN WO2004024885-A2.

XX

PD 25-MAR-2004.

XX

PF 15-SEP-2003; 2003WO-US028923.

XX

PR 13-SEP-2002; 2002US-0410736P.

XX

PA (CORR) CORNELL RES FOUND INC.

XX

PA (USDA) US SEC OF AGRIC.

XX

PI Lei X, Mullane EJ, Ullah AHJ;

XX

DR WPI; 2004-270029/25.

XX

DR P-PSDB; ADL91248.

XX

PT Novel isolated mutant phytase e.g. Phya useful for feeding monogastric animals, improving nutritional value of foodstuffs consumed by animal, in vitro hydrolysis of phytate or improving nutritional value of foodstuffs consumed by humans.

XX PS Claim 7; SEQ ID NO 7; 215pp; English.

XX CC The present invention relates to mutant phytases (I) and their coding

CC sequences (ADL91245-ADL91252, ADL91255-ADL91296, ADL91308 and ADL91309).

CC (I) have altered pH profiles and altered pH optima compared to a

CC corresponding non-mutant phytase. (I) are useful for improving the

CC nutritional value of a feedstuff which involves providing a feedstuff

CC comprising myo-inositol hexakisphosphate, providing (I) and feeding to

CC the animal the feedstuff in combination with (I) under conditions

CC effective to increase the bioavailability of phosphate from phytate. (I)

CC are also useful for feeding a monogastric animal (e.g., fowl species,

CC porcine species, aquatic species, domestic animal chosen from canine

CC species and a feline species, or mammalian species) which involves feeding

CC Oryctolopus, Capra, a Bos, Equus and Ovis species) to the animal. (I) are also useful for

CC feedstuff in combination with (I), to the animal. (I) are also useful for

CC producing specific inositol phosphate metabolites or products for

CC nutritional and biomedical applications. The present sequence is the

CC coding sequence for one such mutant phytase.

XX SQ Sequence 2665 BP; 632 A; 808 C; 575 G; 650 T; 0 U; 0 Other;

Query Match 99.78; Score 1345.4; DB 12; Length 2665;

Best Local Similarity 99.94; Pred. No. 0;

Matches 1346; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CTGGCAGTCCCGGCTCGAGAAATCAATCCAGTTGCGATACGGTTCGATCAGGGGTATCAA 63

DB 842 CTGGCAGTCCCGGCTCGAGAAATCAATCCAGTTGCGATACGGTTCGATCAGGGGTATCAA 901

QY 64 TGGTCTCCGAGACTTCGCAATCTTTGGGGTCAATACGACACCGTTCTCTCTCTGGCAAC 123

DB 902 TGGTCTCCGAGACTTCGCAATCTTTGGGGTCAATACGACACCGTTCTCTCTCTGGCAAC 961

QY 124 GAATCGGTGCATCTCCCTGAGGTCCCGCGGATGACAGATGACTTTCGGTTCAGGTCCCTC 183

DB 962 GAATCGGTGCATCTCCCTGAGGTCCCGCGGATGACAGATGACTTTCGGTTCAGGTCCCTC 1021

QY 184 TCCCGTTCATGAGCGCGGTATCCGACCGACTCCGAGGCAAGAAATATCCCGTCTCATTT 243

DB 1022 TCCCGTTCATGAGCGCGGTATCCGACCGACTCCGAGGCAAGAAATATCCCGTCTCATTT 1081

QY 244 GAGGAGATCCGACGAGCGGACCGACCTTTGACGGAATATGCTTCTTGAGACATAC 303

DB 1082 GAGGAGATCCGACGAGCGGACCGACCTTTGACGGAATATGCTTCTTGAGACATAC 1141

QY 304 AACTACAGCTTGGGTGAGATGACCTGACTCCCTTCGGAGAACAGAGAGTGTCAACTCC 363

DB 1142 AACTACAGCTTGGGTGAGATGACCTGACTCCCTTCGGAGAACAGAGAGTGTCAACTCC 1201

QY 364 GGCATCAAGTTCTACCGAGGTGCAATCGGTGCAAGGAACATCGTTCCATTTCATCCGA 423

DB 1202 GGCATCAAGTTCTACCGAGGTGCAATCGGTGCAAGGAACATCGTTCCATTTCATCCGA 1261

QY 424 TCCCTGCTCCAGCGGTGATCGCTCCGGCAAGAAATTCATCGAGGGCTTCGAGC 483

DB 1262 TCCCTGCTCCAGCGGTGATCGCTCCGGCAAGAAATTCATCGAGGGCTTCGAGC 1321

QY 484 ACCAAGCTGAAGGATCTCTGTCGCCAGCCCGGCCCAATGTCGCCCAAGATCGAGTGGTC 543

DB 1322 ACCAAGCTGAAGGATCTCTGTCGCCAGCCCGGCCCAATGTCGCCCAAGATCGAGTGGTC 1381

QY 544 ATTTCCGAGCGGAGTCAATCAACACACTCTCGACCCAGGCACTGCTGCTTCGAA 603

DB 1382 ATTTCCGAGCGGAGTCAATCAACACACTCTCGACCCAGGCACTGCTGCTTCGAA 1441

QY 604 GACAGCAATTTGGCGATACCGTTCGAGCCCAATTTCAACCGCAGCTTTCCTCCATTT 663

DB 1442 GACAGCAATTTGGCGATACCGTTCGAGCCCAATTTCAACCGCAGCTTTCCTCCATTT 1501

QY 664 CGTCAACGTCGTGAGAACGACCTGTCGGGTGACTCTCAGACAGACAGAGTGCACCTAC 723

DB 1502 CGTCAACGTCGTGAGAACGACCTGTCGGGTGACTCTCAGACAGACAGAGTGCACCTAC 1561

QY 724 CTCATGACATGTGCTCCTTCGACACCAATCTCCACGACCGTCGACACCAAGCTGTCC 783

DB 1562 CTCATGACATGTGCTCCTTCGACACCAATCTCCACGACCGTCGACACCAAGCTGTCC 1621

QY 784 CCCTTCTGTGACCTGTGTTACCCATGACGAATGGATCACTACGACTACCTCCAGTCCCTTG 843

DB 1622 CCCTTCTGTGACCTGTGTTACCCATGACGAATGGATCACTACGACTACCTCCAGTCCCTTG 1681

QY 844 AAAAGATATTACGGCAGTGTGCGAGTAAACCCGCTCGGCCCGGACCCAGGGGCTGGCTAC 903

DB 1682 GAAAAGTATTACGGCAGTGTGCGAGTAAACCCGCTCGGCCCGGACCCAGGGGCTGGCTAC 1741

QY 904 GCTAACGAGCTCATCGCCGCTGTGACCCACTCGGCTGTCCAGATGACACCAAGTCCCAAC 963

DB 1742 GCTAACGAGCTCATCGCCGCTGTGACCCACTCGGCTGTCCAGATGACACCAAGTCCCAAC 1801

QY 964 CACACTTTGGACTCGAGCCCGGCTACCTTTCCGCTCAACTCTCTCTACGCGACTTT 1023

DB 1802 CACACTTTGGACTCGAGCCCGGCTACCTTTCCGCTCAACTCTCTCTCTACGCGACTTT 1861

QY 1024 TCGCATGACACGGCATCATCTCCATTTCTTTGTTAGTCTGTACACGGCACTAAG 1083

DB 1862 TCGCATGACACGGCATCATCTCCATTTCTTTGTTAGTCTGTACACGGCACTAAG 1921

QY 1084 CCGCTATCTACACGACCGTGGAGATATCACCCAGACAGATGGATTTCTCGTCTGCTTGG 1143

DB 1922 CCGCTATCTACACGACCGTGGAGATATCACCCAGACAGATGGATTTCTCGTCTGCTTGG 1981

QY 1144 ACGGTTCCGTTTGTCTTCGCTTTGTACGTCGAGATGATGTCAGTGTGTCAGGCGGAGCAGG 1203

DB 1982 ACGGTTCCGTTTGTCTTCGCTTTGTACGTCGAGATGATGTCAGTGTGTCAGGCGGAGCAGG 2041

QY 1204 CCGCTGGTCCGCTGCTTGGTTAATGATCGGTTGTCGCTGTCATGCGGTGTCGCTTGCAT 1263

DB 2042 CCGCTGGTCCGCTGCTTGGTTAATGATCGGTTGTCGCTGTCATGCGGTGTCGCTTGCAT 2101

QY 1264 GCTTTGGGAGATGACCCGGGATAGCTTTGTGAGGGGTTGAGCTTTGCTAGATCTGGG 1323

DB 2102 GCTTTGGGAGATGACCCGGGATAGCTTTGTGAGGGGTTGAGCTTTGCTAGATCTGGG 2161

QY 1324 GGTGATTTGGCGGAGTGTTTTTCCTTAG 1350

DB 2162 GGTGATTTGGCGGAGTGTTTTTCCTTAG 2188

RESULT 14

ADL91251

ID ADL91251 standard; DNA; 2665 BP.

XX AC ADL91251;

XX AC ADL91251;

XX DT 17-JUN-2004 (first entry)

XX DE Mutant phytase, Q50L, coding sequence, SEQ ID 11.

XX KW Mutant; mutein; phytase; enzyme; foodstuff; animal feed;

XX KW inositol phosphate; gene; ds.

XX OS Aspergillus niger.

XX OS Synthetic.

XX PN WO2004024885-A2.

XX PD 25-MAR-2004.

XX PF 15-SEP-2003; 2003WO-US028923.

XX PR 13-SEP-2002; 2002US-0410736P.

XX PA (CORR) CORNELL RES FOUND INC.

XX PA (USDA) US SEC OF AGRIC.

PD 25-MAR-2004.
XX
PF 15-SEP-2003; 2003WO-US028923.
XX
PR 13-SEP-2002; 2002US-0410736P.
XX
XX (CORR) CORNELL RES FOUND INC.
PA (USDA) US SEC OF AGRIC.
XX
XX Lei X, Mullaney EJ, Ullah AHJ;
XX
XX WPI; 2004-270029/25.
DR
DR P-PSDB; ADL91260.
XX
XX Novel isolated mutant phytase e.g. PhYA useful for feeding monogastric
PT animals, improving nutritional value of foodstuffs consumed by animal, in
PT vitro hydrolysis of phytate or improving nutritional value of foodstuffs
PT consumed by humans.
XX
XX Claim 4; SEQ ID NO 19; 215pp; English.
XX
XX The present invention relates to mutant phytases (I) and their coding
CC sequences (ADL91245-ADL91252, ADL91255-ADL91296, ADL91308 and ADL91309).
CC (I) have altered pH profiles and altered pH optima compared to a
CC corresponding non-mutant phytase. (I) are useful for improving the
CC nutritional value of a foodstuff which involves providing a foodstuff
CC comprising myo-inositol hexakisphosphate, providing (I) and feeding to
CC the animal the foodstuff in combination with (I) under conditions
CC effective to increase the bioavailability of phosphate from phytate. (I)
CC are also useful for feeding a monogastric animal (e.g., fowl species,
CC porcine species, aquatic species, domestic animal chosen from canine
CC species and a feline species, or mammalian species chosen from
CC Oryctolagus, Capra, a Bos, Equus and Ovis species) which involves feeding
CC foodstuff in combination with (I), to the animal. (I) are also useful for
CC producing specific inositol phosphate metabolites or products for
CC nutritional and biomedical applications. The present sequence is the
CC coding sequence for one such mutant phytase.
XX
XX Sequence 2665 BP; 632 A; 808 C; 575 G; 650 T; 0 U; 0 Other;
Query Match 99.7%; Score 1345.4; DB 12; Length 2665;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1346; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 4 CTGGAGTCCCGCGCTCGAGAAATCAATCCAGTTCGATACGTCGATCGGGGTATCAA 63
Db 842 CTGGAGTCCCGCGCTCGAGAAATCAATCCAGTTCGATACGTCGATCGGGGTATCAA 901
Oy 64 TGCTTCTCCGAGACTTCGCATCTTTGGGGTCAATACGACCGCTTCTTCTCTCGGCAAC 123
Db 902 TGCTTCTCCGAGACTTCGCATCTTTGGGGTCAATACGACCGCTTCTTCTCTCGGCAAC 961
Oy 124 GAATCGGTCACTCCCTCGAGGTGCGCCCGCGATGCGAGTCACTTTTCGTCAGGTCTC 183
Db 962 GAATCGGTCACTCCCTCGAGGTGCGCCCGCGATGCGAGTCACTTTTCGTCAGGTCTC 1021
Oy 184 TCCGTCATGAGCGCGGTATCCGACCGACTCCAGGCAAGAAATATCCCGTCTCAT 243
Db 1022 TCCGTCATGAGCGCGGTATCCGACCGACTCCAGGCAAGAAATATCCCGTCTCAT 1081
Oy 244 GAGGAGATCCAGCAGAACCGACCACTTTGACGGAAATATGCTTCTCGAAGACATAC 303
Db 1082 GAGGAGATCCAGCAGAACCGACCACTTTGACGGAAATATGCTTCTCGAAGACATAC 1141
Oy 304 AACTACAGTTCGGTGCAGATGACTGACTCCCTTCGGAGAACAGGAGTCACTCC 363
Db 1142 AACTACAGTTCGGTGCAGATGACTGACTCCCTTCGGAGAACAGGAGTCACTCC 1201
Oy 364 GGCATCAAGTTCTACACGGGTACGAATCGTCTCAAGGAAACATCGTTCCATCCGA 423
Db 1202 GGCATCAAGTTCTACACGGGTACGAATCGTCTCAAGGAAACATCGTTCCATCCGA 1261
Oy 424 TCCTCTGGCTCCAGCCGGTGATCGCTCCGGCAAGAAATTCATCGAGGGCTTCAGAGC 483

Db 1262 TCCTCTGGCTCCAGCCGGTGATCGCTCCGGCAAGAAATTCATCGAGGGCTTCAGAGC 1321
Oy 484 ACCAAGCTGAAGGATCTCGTGCAGCCCGGCAATCGTCGCCCAAGATCGAGCTGTC 543
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Oy 544 ATTTCCGAGGCGAGCTCATCAACAACTCTCGACCAGGCACTGCTGCTGCTTTCGAA 603
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Oy 664 CGTCAACGCTCTGGAGAACGACCTGTCGGTGTGACTCTCACAGACACAGAAAGTACCTAC 723
Db 1502 CGTCAACGCTCTGGAGAACGACCTGTCGGTGTGACTCTCACAGACACAGAAAGTACCTAC 1561
Oy 724 CTCATGGACATGTGCTCCTTGGACACCAATCTCCACAGCAGCGTGCAGACCAAGCTGCC 783
Db 1562 CTCATGGACATGTGCTCCTTGGACACCAATCTCCACAGCAGCGTGCAGACCAAGCTGCC 1621
Oy 784 CCCTTCTGTGACTGTTCACCCCATGCAATGGATCAACTACGACTACTCCAGTCTCTG 843
Db 1622 CCCTTCTGTGACTGTTCACCCCATGCAATGGATCAACTACGACTACTCCAGTCTCTG 1681
Oy 844 AAAAGTATTACGGGCATGTGTCAGGTAAACCGCTCGGCCGACCCAGGGGCTCGGCTAC 903
Db 1682 AAAAGTATTACGGGCATGTGTCAGGTAAACCGCTCGGCCGACCCAGGGGCTCGGCTAC 1741
Oy 904 GCTACGAGCTCATCGCGCTGACCCACTCGCTGTCCAGATGACACCAAGTTCACAC 963
Db 1742 GCTACGAGCTCATCGCGCTGACCCACTCGCTGTCCAGATGACACCAAGTTCACAC 1801
Oy 964 CACACTTTGGACTCGAGCCCGCTACTCTTCGGCTCAACTCTACTCTCTACGCGACTTT 1023
Db 1802 CACACTTTGGACTCGAGCCCGCTACTCTTCGGCTCAACTCTACTCTCTACGCGACTTT 1861
Oy 1024 TGCATGACAAAGGCATCATCTCCATCTCTTTGCTTTAGTCTGTACAAAGGCTACAG 1083
Db 1862 TGCATGACAAAGGCATCATCTCCATCTCTTTGCTTTAGTCTGTACAAAGGCTACAG 1921
Oy 1084 CGCTATCTACCAAGACCGTGGAGAAATATCACCCAGACAGATGGATTTCTGCTGCTGG 1143
Db 1922 CGCTATCTACCAAGACCGTGGAGAAATATCACCCAGACAGATGGATTTCTGCTGCTGG 1981
Oy 1144 AGGTTTCCGTTTGGCTTTCGGCTTGTACGTGAGATGATGACGTGTCAGGCGGAGGAG 1203
Db 1982 AGGTTTCCGTTTGGCTTTCGGCTTGTACGTGAGATGATGACGTGTCAGGCGGAGGAG 2041
Oy 1204 CGCTCGCTCGCTGCTTGGTTAATGATCGCTTGTCCCGCTGCATGGGTGTCCGGTTGAT 1263
Db 2042 CGCTCGCTCGCTGCTTGGTTAATGATCGCTTGTCCCGCTGCATGGGTGTCCGGTTGAT 2101
Oy 1264 GCTTTGGGAGATGTATCCCGGATAGCTTTGTAGGGGGTTGAGCTTGTCTAGATCTGG 1323
Db 2102 GCTTTGGGAGATGTATCCCGGATAGCTTTGTAGGGGGTTGAGCTTGTCTAGATCTGG 2161
Oy 1324 GGTGATTTGGCGGAGTGTTCCTTTAG 1350
Db 2162 GGTGATTTGGCGGAGTGTTCCTTTAG 2188

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Job time : 731 secs

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OM nucleic - nucleic search, using sw model

Run on: November 24, 2004, 07:36:37 ; Search time 134 Seconds
(without alignments)
7160.933 Million cell updates/sec

Title: US-10-089-364-3
Perfect score: 1350
Sequence: 1 atgtgcagctcccccctc.....ggcgagtgctttgttag 1350

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 35539441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1347	99.8	1404	1	US-08-693-709-1
4	1347	99.8	1404	2	US-08-419-448-33
5	1347	99.8	1404	3	US-09-233-510-33
6	1347	99.8	6756	1	US-08-151-574-31
7	1347	99.8	6756	2	US-08-419-448-31
8	1347	99.8	6756	3	US-09-233-510-31
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13	1182.2	87.6	1515	3	US-09-543-744-5
14	1182.2	87.6	1515	4	US-09-929-060-5
15	1167.2	86.5	1332	3	US-09-153-855-4
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19	810.4	60.0	1912	3	US-08-744-231-11
20	810.4	60.0	1912	4	US-09-635-504-11
21	659.8	48.9	1426	4	US-09-684-855-168
22	659.8	48.9	1426	4	US-09-488-265B-34
23	636.2	47.1	1567	3	US-08-868-435-34
24	636.2	47.1	1567	3	US-08-744-231-34
25	636.2	47.1	1567	3	US-09-044-718-13
26	636.2	47.1	1567	4	US-09-635-504-34
27	636.2	47.1	1567	4	US-10-062-848-13

28	621.4	46.0	1404	4	US-09-684-855-162	Sequence 162, Appl
29	621.4	46.0	1404	4	US-09-498-265B-28	Sequence 28, Appl
30	613.4	45.4	1426	3	US-08-121-425-3	Sequence 3, Appl
31	613.4	45.4	1426	4	US-09-634-493A-3	Sequence 3, Appl
32	613.4	45.4	1426	4	US-09-684-855-117	Sequence 117, Appl
33	613.4	45.4	1426	4	US-09-488-265B-15	Sequence 15, Appl
34	611.8	45.3	1404	4	US-09-488-265B-90	Sequence 90, Appl
35	608.6	45.1	1404	4	US-09-488-265B-92	Sequence 92, Appl
36	608.6	45.1	1426	4	US-09-684-855-140	Sequence 140, Appl
37	608.6	45.1	1426	4	US-09-488-265B-25	Sequence 25, Appl
38	602	44.6	1404	4	US-09-684-855-164	Sequence 164, Appl
39	602	44.6	1404	4	US-09-488-265B-30	Sequence 30, Appl
40	600	44.4	1404	4	US-09-684-855-166	Sequence 166, Appl
41	600	44.4	1404	4	US-09-488-265B-32	Sequence 32, Appl
42	599	44.4	1404	4	US-09-488-265B-94	Sequence 94, Appl
43	598.4	44.3	1571	3	US-08-868-435-32	Sequence 32, Appl
44	598.4	44.3	1571	3	US-08-744-231-32	Sequence 32, Appl
45	598.4	44.3	1571	3	US-09-044-718-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-08-151-574-33
; Sequence 33, Application US/08151574
; Patent No. 5436156
; GENERAL INFORMATION:
; APPLICANT: Robert F.M. Van Gorcom
; APPLICANT: Willem Van Hartingsveldt
; APPLICANT: Petrus A. Van Paridon
; APPLICANT: Annemarie E. Veenstra
; APPLICANT: Rudolf G.M. Luttin
; APPLICANT: Gerardus Selden
; TITLE OF INVENTION: Cloning and Expression of Microbial
; TITLE OF INVENTION: Phytase
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025-3471
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/151,574
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/688,578
; FILING DATE: 24-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20026.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1404 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:

ORGANISM: *Aspergillus ficum* (*Aspergillus niger*)
STRAIN: NRRL 3135
US-08-151-574-33

Query Match 99.8%; Score 1347; DB 1; Length 1404;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 184 TCCCTCATGAGCGGGTATCCGACCGACTCCAGGSCAAGAAATCTCCGCTCTCAT 243
DB 238 TCCCTCATGAGCGGGTATCCGACCGACTCCAGGSCAAGAAATCTCCGCTCTCAT 297
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DB 298 GAGGAGATCCAGCAGAACCGGACCACTTTGACGGAAATATGCTTCTCAAGACATAC 357
QY 304 AACTACAGTTGGGTGAGATGACTGCTCTCCCTCGGAGAACAGGAGTAGTCAATCC 363
DB 358 AACTACAGTTGGGTGAGATGACTGCTCTCCCTCGGAGAACAGGAGTAGTCAATCC 417
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QY 424 TCCTCTGCTCCAGCGCGTATCGCTCCGCGAAGAAATTCATCGAGGGCTTCAGAGC 483
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QY 484 ACCAGCTGAGAGTCTCTGCGCCAGCGCGGCAATCGTCCGCGAAGTCAAGTGGTC 543
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QY 544 ATTTCCGAGGCGAGTCAATCAACAACTCTCGACCCAGGACCTGCACTGCTTCGAA 603
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QY 664 CGTCAAGTCTGGAGAACGACTCTCGGTGTGACTCTCAGACACAGAAAGTCACTAC 723
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DB 898 AAAAGATTATCGGCCATGTGAGGTAAACCGCTCGGCCCGACCCAGGCGCTCGCTAC 957
QY 904 GCTAACGAGTCAATCGCCCTCTGACCCACTCGCTGTCCAGATGACACGATTCAC 963
DB 958 GCTAACGAGTCAATCGCCCTCTGACCCACTCGCTGTCCAGATGACACGATTCAC 1017
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DB 1018 CACACTTGGACTCGAGCCGGCTACCTTTCCGCTCAACTCTACTCTACCGGACTTT 1077
QY 1024 TCCCATGACAAACGGCATCATCTCCATCTCTTTGCTTTAGGCTGTACAAACGGCACTAG 1083
DB 1078 TCCCATGACAAACGGCATCATCTCCATCTCTTTGCTTTAGGCTGTACAAACGGCACTAG 1137
QY 1084 CCCTATCTACCAACGACCGTGGAGAAATATCAACCCAGACAGATGGATTCTCGTCTGCTGG 1143
DB 1138 CCCTATCTACCAACGACCGTGGAGAAATATCAACCCAGACAGATGGATTCTCGTCTGCTGG 1197
QY 1144 ACGTTCCGTTTCTGCTTCCGCTTTGACGTCGAGATGATCCAGTGTCCGCGAGACAGAG 1203
DB 1198 ACGTTCCGTTTCTGCTTCCGCTTTGACGTCGAGATGATCCAGTGTCCGCGAGACAGAG 1257
QY 1204 CCCTCGTCCGTTCTGCTTAAATGATCCGCTTGTCCCGCTCATGGGTGTCCGCTTGTAT 1263
DB 1258 CCCTCGTCCGTTCTGCTTAAATGATCCGCTTGTCCCGCTCATGGGTGTCCGCTTGTAT 1317
QY 1264 GCTTTGGGAGATGTACCCGCGATGACTTTGTGAGGGGTTGAGCTTTGCTAGATCTGG 1323
DB 1318 GCTTTGGGAGATGTACCCGCGATGACTTTGTGAGGGGTTGAGCTTTGCTAGATCTGG 1377
QY 1324 GGTGATTGGCGGAGTGTCTTCTCTAG 1350
DB 1378 GGTGATTGGCGGAGTGTCTTCTCTAG 1404
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RESULT 2

US-08-146-424-19
; Sequence 19, Application US/08146424
; Patent No. 5593963
; GENERAL INFORMATION:
; APPLICANT: VAN COIJEN, ALBERT J. J.
; APPLICANT: RIETVELD, KRIJN
; APPLICANT: HOEKEMA, ANDREAS
; APPLICANT: PEN, JAN
; APPLICANT: SIJMONS, PETER C.
; APPLICANT: VERWOERD, TRUJIS C.
; TITLE OF INVENTION: THE EXPRESSION OF PHYTASE IN PLANTS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146,424
; FILING DATE: 02-NOV-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: KENNEDY, BILL
; REGISTRATION NUMBER: 33,407
; REFERENCE/DOCKET NUMBER: 44615-20011.24
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1404 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS

		LOCATION: 1..1401		99.8%; Score 1347; DB 1; Length 1404;	
		FEATURE: mat_peptide		Best Local Similarity 100.0%; Pred. No. 0;	
		LOCATION: 70		Matches 1347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
		US-08-146-424-19			
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QY	64	TGCTTCTCCGAGATTGCGATCTTTGGGGTCAATACGACCGTTCCTCTCTGCGCAAC	123		
Db	118	TGCTTCTCCGAGATTGCGATCTTTGGGGTCAATACGACCGTTCCTCTCTGCGCAAC	177		
QY	124	GAATCGGTATCTCCCTGAGGTGCGCGCGATGACAGTCACTTTCCGTCAGGTCTCTC	183		
Db	178	GAATCGGTATCTCCCTGAGGTGCGCGCGATGACAGTCACTTTCCGTCAGGTCTCTC	237		
QY	184	TCCCGTCATGAGCGCGGTATCCGACCGACTCCAAGGGCAAGAAATATCTCCGCTCTCAT	243		
Db	238	TCCCGTCATGAGCGCGGTATCCGACCGACTCCAAGGGCAAGAAATATCTCCGCTCTCAT	297		
QY	244	GAGGAGATCCAGCAGAACCGGACCACTTTGACGGAATAATGCTTCTCGAGAGATAC	303		
Db	298	GAGGAGATCCAGCAGAACCGGACCACTTTGACGGAATAATGCTTCTCGAGAGATAC	357		
QY	304	AACATACAGTCTGGGTGAGATGACCTGACTCCCTTCGGAGAACAGAGAGTGTCAACTCC	363		
Db	358	AACATACAGTCTGGGTGAGATGACCTGACTCCCTTCGGAGAACAGAGAGTGTCAACTCC	417		
QY	364	GGCATCAAGTCTACAGCGGTAGCAATCGTCAAGGAACATCGTTCATTCATCCGA	423		
Db	418	GGCATCAAGTCTACAGCGGTAGCAATCGTCAAGGAACATCGTTCATTCATCCGA	477		
QY	424	TCCTCTGGCTCCAGCGGTGATCGCTCCGGCAAGAAATTCATCGAGGGCTTCCAGAGC	483		
Db	478	TCCTCTGGCTCCAGCGGTGATCGCTCCGGCAAGAAATTCATCGAGGGCTTCCAGAGC	537		
QY	484	ACCAAGCTGAAGATCTCTGTCGCCAGCCCGGCGCAATCGTGGCCAAAGATCGAGTGGTC	543		
Db	538	ACCAAGCTGAAGATCTCTGTCGCCAGCCCGGCGCAATCGTGGCCAAAGATCGAGTGGTC	597		
QY	544	ATTTCCGAGGCGAGTCAATCCAAACACTCTGACCCAGGACCTGACTGTCTTCGAA	603		
Db	598	ATTTCCGAGGCGAGTCAATCCAAACACTCTGACCCAGGACCTGACTGTCTTCGAA	657		
QY	604	GACAGCGAATTGGCGGATACCGTGAAGCCCAATTTACCGCCAGTTCGTCCTCCCAT	663		
Db	658	GACAGCGAATTGGCGGATACCGTGAAGCCCAATTTACCGCCAGTTCGTCCTCCCAT	717		
QY	664	CGTCAACGCTTGGAGAACGACTGTCTCCGGTGTGACTCTCACAGACACAGAGTACCTAC	723		
Db	718	CGTCAACGCTTGGAGAACGACTGTCTCCGGTGTGACTCTCACAGACACAGAGTACCTAC	777		
QY	724	CTCATGGACATGTCTCTCTCGACACCATCTCCACGACCGCTCGACCAAGCTGTCC	783		
Db	778	CTCATGGACATGTCTCTCTCGACACCATCTCCACGACCGCTCGACCAAGCTGTCC	837		
QY	784	CCCTTCTGTGACCTGTTCCACCATGACGAATGGATCAACTAGACTACCTCCAGTCTCTG	843		
Db	838	CCCTTCTGTGACCTGTTCCACCATGACGAATGGATCAACTAGACTACCTCCAGTCTCTG	897		
QY	844	AAAAAGTATTACGGCATGTGAGTAACCGGTCCGCCCGACCCAGGGGCTCGGTAC	903		
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QY	904	GCTAACGAGCTCATCGCCCGTCTGACCCCACTCGCCTGTCCAGATGACACAGTCCCAAC	963		
Db	958	GCTAACGAGCTCATCGCCCGTCTGACCCCACTCGCCTGTCCAGATGACACAGTCCCAAC	1017		

RESULT 3
US-08-693-709-1
; Sequence 1, Application US/08693709
; Patent No. 5770413
; GENERAL INFORMATION:
; APPLICANT: VAN COIJEN, ALBERT J.J.
; APPLICANT: RIETVELD, KRIJN
; APPLICANT: HOEKENA, ANDREAS
; APPLICANT: PEN, JAN
; APPLICANT: SIJMONS, PETER C.
; APPLICANT: VERWOERD, TEUNIS C.
; TITLE OF INVENTION: THE EXPRESSION OF PHYTASE
; TITLE OF INVENTION: IN PLANTS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/693,709
; FILING DATE: 07-AUG-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146,424
; FILING DATE: 02-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20011.10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:

QY	964	CACACTTTGGACTCGAGCCGGCTACCTTCCGCTCAACTCTACTCTCTCTAGCGGACTTT	1023
Db	1018	CACACTTTGGACTCGAGCCGGCTACCTTCCGCTCAACTCTACTCTCTCTAGCGGACTTT	1077
QY	1024	TCCGATGACAAACGGCATCATCTCCATCTCTTTAGTCTGTGTACAAACGGCACTAAG	1083
Db	1078	TCCGATGACAAACGGCATCATCTCCATCTCTTTAGTCTGTGTACAAACGGCACTAAG	1137
QY	1084	CCGCTATCTACACACCGTGGAGAAATATCAACAGAGATGATCTCGTCTGCTTGG	1143
Db	1138	CCGCTATCTACACACCGTGGAGAAATATCAACAGAGATGATCTCGTCTGCTTGG	1197
QY	1144	ACGGTTCCGTTTGGCTTCGCGTTTGTACGTCGAGATGATGACGCGGAGCAGGAG	1203
Db	1198	ACGGTTCCGTTTGGCTTCGCGTTTGTACGTCGAGATGATGACGCGGAGCAGGAG	1257
QY	1204	CCGCTGGTCCGTTTGGTAAATGATCGCGTTTCCCGCTGCATGGTGTCCGTTGAT	1263
Db	1258	CCGCTGGTCCGTTTGGTAAATGATCGCGTTTCCCGCTGCATGGTGTCCGTTGAT	1317
QY	1264	GCTTTGGGAGATGATACCGGGATAGCTTGTGAGGGGGTTGAGCTTTGCTAGATCTCGG	1323
Db	1318	GCTTTGGGAGATGATACCGGGATAGCTTGTGAGGGGGTTGAGCTTTGCTAGATCTCGG	1377
QY	1324	GCTGATTGGCGGAGTGTTCCTTAG	1350
Db	1378	GCTGATTGGCGGAGTGTTCCTTAG	1404

/ LENGTH: 1404 base pairs
 / TYPE: nucleic acid
 / STRANDEDNESS: double
 / TOPOLOGY: linear
 / FEATURE:
 / NAME/KEY: Coding Sequence
 / LOCATION: 1...1401
 / OTHER INFORMATION:
 / NAME/KEY: mat_peptide
 / LOCATION: 70...1401
 / OTHER INFORMATION:
 / NAME/KEY: Signal Sequence
 / LOCATION: 1...72
 / OTHER INFORMATION:
 / US-08-693-709-1

Query Match 99.8%; Score 1347; DB 1; Length 1404;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	4	CTGGCAGTCCCGCTCGAGAAATCAATCCAGTTCGATACGGTCGATPCAGGGGTATCAA	63
Db	58	CTGGCAGTCCCGCTCGAGAAATCAATCCAGTTCGATACGGTCGATPCAGGGGTATCAA	117
QY	64	TGCTTCTCGAGACTTCGATCTTTGGGGTCAATACGACCGTTCCTCTCTCGCAAC	123
Db	118	TGCTTCTCGAGACTTCGATCTTTGGGGTCAATACGACCGTTCCTCTCTCGCAAC	177
QY	124	GAATCGGTCACTCCCTGAGTGCCTCGCGGATGAGAGTCACTTCGCTCAGGTCTC	183
Db	178	GAATCGGTCACTCCCTGAGTGCCTCGCGGATGAGAGTCACTTCGCTCAGGTCTC	237
QY	184	TCCGTCATGAGCGGTATCCGACGACTCCAGGCGAAGAAATACCTCGCTCTCAT	243
Db	238	TCCGTCATGAGCGGTATCCGACGACTCCAGGCGAAGAAATACCTCGCTCTCAT	297
QY	244	GAGGAGATCCAGCAACGCGACCACTTTGACGGAAATATGCTTCCTGAGACATAC	303
Db	298	GAGGAGATCCAGCAACGCGACCACTTTGACGGAAATATGCTTCCTGAGACATAC	357
QY	304	AATACAGCTTGGTGCAGATGACTGACTCCCTTCGGAGAACAGGAGTAGTCACTCC	363
Db	358	AATACAGCTTGGTGCAGATGACTGACTCCCTTCGGAGAACAGGAGTAGTCACTCC	417
QY	364	GGCATCAAGTTCTACACGCGTACGAATCGCTCAAGGAAACATCGTTCCATTCAACGA	423
Db	418	GGCATCAAGTTCTACACGCGTACGAATCGCTCAAGGAAACATCGTTCCATTCAACGA	477
QY	424	TCCTCTGCTCCAGCGCGTATCGCTTCGGCAAGAAATTCATCGAGGCTTCCAGAGC	483
Db	478	TCCTCTGCTCCAGCGCGTATCGCTTCGGCAAGAAATTCATCGAGGCTTCCAGAGC	537
QY	484	ACCAAGCTGAAGGATCTCTGCGCCAGCCGCGCAATCGTCGCCAGATCGAGTGGTC	543
Db	538	ACCAAGCTGAAGGATCTCTGCGCCAGCCGCGCAATCGTCGCCAGATCGAGTGGTC	597
QY	544	ATTTCCGAGGCGAGTCAATCAACAACTCTCGACCCAGGACCTGCTGCTCGAA	603
Db	598	ATTTCCGAGGCGAGTCAATCAACAACTCTCGACCCAGGACCTGCTGCTCGAA	657
QY	604	GACAGCAATTTGGCGGATACCGTCGAGCAATTTCAACCGCAAGTTCGTCCTCCAT	663
Db	658	GACAGCAATTTGGCGGATACCGTCGAGCAATTTCAACCGCAAGTTCGTCCTCCAT	717
QY	664	CGTCAACGCTTGGAGACGACCTCTCGGTGTGACTCTCACAGACAGAAAGTCACTAC	723
Db	718	CGTCAACGCTTGGAGACGACCTCTCGGTGTGACTCTCACAGACAGAAAGTCACTAC	777
QY	724	CTCATGACATGTCTCTTCGACACCATCTCCACCGACCGTTCGACACCAAGTGTCC	783
Db	778	CTCATGACATGTCTCTTCGACACCATCTCCACCGACCGTTCGACACCAAGTGTCC	837
QY	784	CCCTTCTGTGACCTGTTTCAACCCATGACGAATGGATCAACTACGACTACCTCCAGTCTTG	843

Db	838	CCCTTCTGTGACCTGTTTCAACCCATGACGAATGATCACTACGACTACCTCCAGTCTTG	897
QY	844	AAAAGTATTACGGCCATGTCAGTAACCCGCTCGGCCCGACCCAGGGGTCGCGTAC	903
Db	898	AAAAGTATTACGGCCATGTCAGTAACCCGCTCGGCCCGACCCAGGGGTCGCGTAC	957
QY	904	GCTAACGAGCTCATCGCCGCTCTGACCCACTCGCCCTGTCCACGATGACACCAAGTCCAAAC	963
Db	958	GCTAACGAGCTCATCGCCGCTCTGACCCACTCGCCCTGTCCACGATGACACCAAGTCCAAAC	1017
QY	964	CACACTTTGAGACTCGAGCCCGGCTACCTTTCCGCTCAACTCTCTACCGGACTTT	1023
Db	1018	CACACTTTGAGACTCGAGCCCGGCTACCTTTCCGCTCAACTCTCTACCGGACTTT	1077
QY	1024	TGCGATGACAAAGGATCATCTCCATTCCTTTAGTCTGTACAAAGGCACTAAG	1083
Db	1078	TGCGATGACAAAGGATCATCTCCATTCCTTTAGTCTGTACAAAGGCACTAAG	1137
QY	1084	CCGCTATCTACCAAGCAGCTGAGAAATATACCCAGACAGATGGAATCTCGTCTCTTG	1143
Db	1138	CCGCTATCTACCAAGCAGCTGAGAAATATACCCAGACAGATGGAATCTCGTCTCTTG	1197
QY	1144	ACGTTTCCGTTTGTTCGGGTTGTACGTCGAGATGATGCAAGTGTACGCGGAGCAGGAG	1203
Db	1198	ACGTTTCCGTTTGTTCGGGTTGTACGTCGAGATGATGCAAGTGTACGCGGAGCAGGAG	1257
QY	1204	CCGCTGCTCGTCTCTGTTAATGATCGGTTGTCCGCTGCATGCGGTTCGGTTCGAT	1263
Db	1258	CCGCTGCTCGTCTCTGTTAATGATCGGTTGTCCGCTGCATGCGGTTCGAT	1317
QY	1264	GCTTTGGGAGATGTACCCGGATGACTTTGTAGGGGTTGAGCTTGTCTAGATCTGGG	1323
Db	1318	GCTTTGGGAGATGTACCCGGATGACTTTGTAGGGGTTGAGCTTGTCTAGATCTGGG	1377
QY	1324	GCTGATTGGCGGAGTGTTCCTTAG	1350
Db	1378	GCTGATTGGCGGAGTGTTCCTTAG	1404

RESULT 4
 US-08-419-448-33
 ; Sequence 33, Application US/08419448
 ; Patent No. 5863533
 ; GENERAL INFORMATION:
 ; APPLICANT: Robert F.M. Van Gorkom
 ; APPLICANT: Willem Van Hartingsveldt
 ; APPLICANT: Petrus A. Van Paridon
 ; APPLICANT: Annemarie E. Veenstra
 ; APPLICANT: Rudolf G.M. Luttin
 ; APPLICANT: Gerardus Selten
 ; TITLE OF INVENTION: Cloning and Expression of Microbial
 ; TITLE OF INVENTION: Phytase
 ; NUMBER OF SEQUENCES: 52
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Morrison & Foerster
 ; STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20006-1888
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/419,448
 ; FILING DATE: 10-APR-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Murashige, Kate H.

REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 24615-20026.10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 1404 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Aspergillus ficuum (Aspergillus niger)
STRAIN: NREL 3135
US-08-419-448-33

Query Match 99.8%; Score 1347; DB 2; Length 1404;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CTGACGATCCCGCTCGAGAAATCAATCCAGTTGCGATACGFTCGATCAGGGGTATCAA 63
Db 58 CTGACGATCCCGCTCGAGAAATCAATCCAGTTGCGATACGFTCGATCAGGGGTATCAA 117
QY 64 TGCTTCTCCGAGACTTCGATCTTTGGGTCATACGACCGTTCTTCTCTCTGGCAAC 123
Db 118 TGCTTCTCCGAGACTTCGATCTTTGGGTCATACGACCGTTCTTCTCTCTGGCAAC 177
QY 124 GAATCGGTATCTCCCTGAGGTGCCCGCGGATGACAGTCACTTTTCGTCAGGTCCTC 183
Db 178 GAATCGGTATCTCCCTGAGGTGCCCGCGGATGACAGTCACTTTTCGTCAGGTCCTC 237
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Db 298 GAGGAGATCCAGCAGAACGCGACCACTTTGACGGAATAATGCTTCTCTGAAGACATAC 357
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Db 358 AACTACAGTTGGTGCAGATGACCTGACTCCCTTCGGAAGAACAGGAGTGTCACTCC 417
QY 364 GGCATCAAGTTCTACGAGCGGTACGATCGCTCAAGGACATCGTTCATTCATCCGA 423
Db 418 GGCATCAAGTTCTACGAGCGGTACGATCGCTCAAGGACATCGTTCATTCATCCGA 477
QY 424 TCCTCTGCTCCAGCGCGTATCGCTCCGCGCAAGAAATTCATCGAGGGCTTCCAGAGC 483
Db 478 TCCTCTGCTCCAGCGCGTATCGCTCCGCGCAAGAAATTCATCGAGGGCTTCCAGAGC 537
QY 484 ACCAAGTGAAGGATCTCTGTCGCGAGCGCGGCAATCGTCCGCAAGATCGAGTGGTC 543
Db 538 ACCAAGTGAAGGATCTCTGTCGCGAGCGCGGCAATCGTCCGCAAGATCGAGTGGTC 597
QY 544 ATTTCCGAGGCGAGTCTATCAACAACTCTGACCCAGGCACTGCTGCTTCGAA 603
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Db 718 CGTCAAGCTCGGAGAACGCTGTCGCGTGTGACTCTCACAGACAGAGAGTCACTAC 777
QY 724 CTCATGACATGTGCTCTTCGACACCACTCTCCACGACCGTCCGACCAAGCTGCC 783
Db 778 CTCATGACATGTGCTCTTCGACACCACTCTCCACGACCGTCCGACCAAGCTGCC 837

RESULT 5

US-09-233-510-33
; Sequence 33, Application US/09233510
; Patent No. 6350602
; GENERAL INFORMATION:
; APPLICANT: Robert F.M. Van Gorcom
; APPLICANT: Willem Van Hartingsveldt
; APPLICANT: Petrus A. Van Paridon
; APPLICANT: Anemarie B. Veenstra
; APPLICANT: Rudolf G.M. Luttin
; APPLICANT: Gerardus Selten
; TITLE OF INVENTION: Cloning and Expression of Microbial
; TITLE OF INVENTION: Phytase
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025-3471
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,510
; FILING DATE:
; CLASSIFICATION:

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/688,578
; FILING DATE: 24-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; TELECOMMUNICATION INFORMATION:
; REFERENCE/DOCKET NUMBER: 24615-20026.00
; TELEPHONE: 415-327-7250
; TELEFAX: 415-327-2951
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1404 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Aspergillus ficuum (Aspergillus niger)
; STRAIN: NRRL 3135
; US-09-233-510-33

Query Match          99.8%; Score 1347; DB 3; Length 1404;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CTGGCAGTCCCGCTCGAGAAATCAATCCAGTTGCGATACGGTCGATCAGGGGTATCAA 63
DB 58 CTGGCAGTCCCGCTCGAGAAATCAATCCAGTTGCGATACGGTCGATCAGGGGTATCAA 117
QY 64 TGCTTCTCCGAGACTTCGCATCTTTGGGTCAATACGACCGTCTCTCTCTCGGCAAC 123
DB 118 TGCTTCTCCGAGACTTCGCATCTTTGGGTCAATACGACCGTCTCTCTCTCGGCAAC 177
QY 124 GAATCGGTCAATCCCTCGAGTCCCGCGGATGCGAGTCACTTTGCTCAGGTCTTC 183
DB 178 GAATCGGTCAATCCCTCGAGTCCCGCGGATGCGAGTCACTTTGCTCAGGTCTTC 237
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DB 238 TCCGTCATGAGCGCGTATCCGACCGATCCGAGGCGAAGAAATCTCGCTCTCAAT 297
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RESULT 6

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US-08-151-574-31
; Sequence 31, Application US/08151574
; Patent No. 5436156
; GENERAL INFORMATION:
; APPLICANT: Robert F. M. Van Gorpom
; APPLICANT: Willem Van Hartingsveldt
; APPLICANT: Petrus A. Van Paridon
; APPLICANT: Annemarie E. Veenstra
; APPLICANT: Rudolf G. M. Luttin
; APPLICANT: Gerardus Selten
; TITLE OF INVENTION: Cloning and Expression of Microbial
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025-3471
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWARE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/151,574
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/688,578
FILING DATE: 24-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 24615-20026.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-327-7250
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 6756 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Aspergillus ficum (Aspergillus niger)
STRAIN: NRRL 3135
IMMEDIATE SOURCE:
LIBRARY: lambda AF
CLONE: pAF2-3, pAF2-6, pAF2-7
FEATURE:
NAME/KEY: exon
LOCATION: 210..253
FEATURE:
NAME/KEY: intron
LOCATION: 254..355
FEATURE:
NAME/KEY: exon
LOCATION: 356..1715
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NAME/KEY: CDS
LOCATION: join(210..253, 356..1715)
OTHER INFORMATION: /codon_start= 210
OTHER INFORMATION: /product= "Phytase"
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 210..380
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NAME/KEY: mat_peptide
LOCATION: 381..1712
IDENTIFICATION METHOD: experimental
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OTHER INFORMATION: /product= "Phytase"
OTHER INFORMATION: /evidence= EXPERIMENTAL
US-08-151-574-31

Query Match 99.8%; Score 1347; DB 1; Length 6756;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 CTGGCAGTCCCGCTCGAGAAATCAATCCAGTTGGCATACGGTTCGATCAGGGGTATCAA 63
DB 369 CTGGCAGTCCCGCTCGAGAAATCAATCCAGTTGGCATACGGTTCGATCAGGGGTATCAA 428
QY 64 TGCTTCTCCGAGATTTCGATCTTTGGGTCAATACGACGGTTCCTCTCTGGCAAC 123
DB 429 TGCTTCTCCGAGATTTCGATCTTTGGGTCAATACGACGGTTCCTCTCTGGCAAC 488
QY 124 GAATCGGTCACTCCCTCGAGTCCCGCGGATGCGAGAGTCACTTTCGCTCAGGTCCTC 183
DB 489 GAATCGGTCACTCCCTCGAGTCCCGCGGATGCGAGAGTCACTTTCGCTCAGGTCCTC 548

QY 184 TCCCGTCAATGAGCGCGGTATCCGACCGAGTCCAAAGGGCAAGAAATACTCCGCTCTCAT 243
DB 549 TCCCGTCAATGAGCGCGGTATCCGACCGAGTCCAAAGGGCAAGAAATACTCCGCTCTCAT 608
QY 244 GAGGAGTCCAGCAGAACGGGACCACTTTGACGGAAATATGCTTCTCTGAAGACATAC 303
DB 609 GAGGAGTCCAGCAGAACGGGACCACTTTGACGGAAATATGCTTCTCTGAAGACATAC 668
QY 304 AACTACAGCTTTGGGTGCAGATGACCTGACTCCCTTCGAGAACAGGAGCTAGTCAACTCC 363
DB 669 AACTACAGCTTTGGGTGCAGATGACCTGACTCCCTTCGAGAACAGGAGCTAGTCAACTCC 728
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QY 424 TCCTCTGGCTCCAGCCGCGTATCGCTCCGCGCAAGAAATTCATCGAGGGCTTCAGAGC 483
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DB 849 ACCAAGCTGAAGATCTCTGTCGCCAGCCCGGCAATGTCGCCCAAGATCGAGTGGTC 908
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QY 664 GGTCAACGCTTGGAGACGACCTGTCGGTGTGACTCTCAGACACAGAGATGACCTAC 723
DB 1029 GGTCAACGCTTGGAGACGACCTGTCGGTGTGACTCTCAGACACAGAGATGACCTAC 1088
QY 724 CTCATGACATGTGCTCTTCGACACCACTCTCCAGCACCCTCGACACCAAGCTGCC 783
DB 1089 CTCATGACATGTGCTCTTCGACACCACTCTCCAGCACCCTCGACACCAAGCTGCC 1148
QY 784 CCCTTCTGTGACTGTTCAACCATGACGAATGGATCACTACGACTACCTCCAGTCCCTG 843
DB 1149 CCCTTCTGTGACTGTTCAACCATGACGAATGGATCACTACGACTACCTCCAGTCCCTG 1208
QY 844 AAAAAAGTATTACGGCCATGTGTCAGGTAAACCGCTCGGCCCGGACCCAGGGGCTGGCTAC 903
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QY 964 CACACTTTGGACTCGAGCCCGGCTACCTTCGGCTCAACTCTACTCTCTACGCGACTTT 1023
DB 1329 CACACTTTGGACTCGAGCCCGGCTACCTTCGGCTCAACTCTACTCTCTACGCGACTTT 1388
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QY 1084 CCGCTATCTACCAACACCGGTGGAGATATCACCCAGACAGATGGATTCCTGCTGCTTGG 1143
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QY 1144 ACGGTTCCGTTTGTCTTCGCTTTGTACGTCGAGATGATGCAGTGTTCAGGCGGAGCAGG 1203
DB 1509 ACGGTTCCGTTTGTCTTCGCTTTGTACGTCGAGATGATGCAGTGTTCAGGCGGAGCAGG 1568
QY 1204 CCGCTGTGCGGTCTTGGTTAATGATCGGTTGCCCGCTGCATGGGTGTCGGTTCAT 1263
DB 1569 CCGCTGTGCGGTCTTGGTTAATGATCGGTTGCCCGCTGCATGGGTGTCGGTTCAT 1628
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Db 1629 GCTTTGGGAGATGATACCGGGAGTAGCTTTGTGAGGGGGTTGAGCTTTGCTAGATCTGGG 1688
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Qy 1324 GGTGATTGGCGGAGTGTTTGCTTAG 1350
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Db 1689 GGTGATTGGCGGAGTGTTTGCTTAG 1715
|||||

RESULT 7

US-08-419-448-31
; Sequence 31, Application US/08419448
; Patent No. 5863533
; GENERAL INFORMATION:
; APPLICANT: Robert F.M. Van Gorcom
; APPLICANT: Willem Van Hartingsveldt
; APPLICANT: Petrus A. Van Paridon
; APPLICANT: Annemarie E. Veenstra
; APPLICANT: Rudolf G.M. Luttin
; APPLICANT: Gerardus Selten
; TITLE OF INVENTION: Cloning and Expression of Microbial
; TITLE OF INVENTION: Phytase
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20008-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/419,448
; FILING DATE: 10-APR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20026.10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6756 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Aspergillus ficuum (Aspergillus niger)
; STRAIN: NRRL 3135
; IMMEDIATE SOURCE:
; LIBRARY: lambda AF
; CLONE: pAF2-3, pAF2-6, pAF2-7
; FEATURE:
; NAME/KEY: exon
; LOCATION: 210..253
; FEATURE:
; NAME/KEY: intron
; LOCATION: 254..355
; FEATURE:
; NAME/KEY: exon
; LOCATION: 356..1715
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(210..253, 356..1715)
; OTHER INFORMATION: /codon_start= 210

; OTHER INFORMATION: /product= "Phytase"
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 210..380
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 381..1712
; IDENTIFICATION METHOD: experimental
; OTHER INFORMATION: /function= "inositol phosphate
; OTHER INFORMATION: /product= "Phytase"
; OTHER INFORMATION: /evidence= EXPERIMENTAL
; US-08-419-448-31

Query Match 99.8%; Score 1347; DB 2; Length 6756;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 CTGGCAGTCCCGCCTCGAGAAATCAATCCAGTTGCGATACGGTCGATCAGGGGTATCAA 63
Db CTGGCAGTCCCGCCTCGAGAAATCAATCCAGTTGCGATACGGTCGATCAGGGGTATCAA 428
Qy 64 TCGTTCTCGAGACTTCGCATCTTTGGGGTCAATAACGACCCGTTCTTCTCTGGCAAC 123
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Qy 124 GAATCGGTCACTCCCTGAGTGGTCCGCGGATGCGAGTCACTTTGCTCAGGTCTC 183
Db GAATCGGTCACTCCCTGAGTGGTCCGCGGATGCGAGTCACTTTGCTCAGGTCTC 548
Qy 184 TCCCGTCATGAGCGCGGTATCCGACCGACTCCAAAGGCAAGAAATATCCGCTCTCAT 243
Db TCCCGTCATGAGCGCGGTATCCGACCGACTCCAAAGGCAAGAAATATCCGCTCTCAT 608
Qy 244 GAGGAGATCCAGCAGAACCGACCACTTTGACCGGAAATATGCTTCCTGAACATAC 303
Db GAGGAGATCCAGCAGAACCGACCACTTTGACCGGAAATATGCTTCCTGAACATAC 669
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Qy 604 GACAGCGAATTTGGCCGATACCGTCAAGCCCAATTTCAACCGACGTTGTCCTCCATT 663
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Db CTCATGGACATGTCTCTCTCGACCACTCTCCACCGACCGTTCGACCAAGTGTCC 1148
Qy 784 CCCTTCTGTGACCTGTTCAACCCATGAGATGATCACTACGACTACCTCCAGTCTTG 843
Db CCCTTCTGTGACCTGTTCAACCCATGAGATGATCACTACGACTACCTCCAGTCTTG 1208

DB 669 AACTACAGCTTTGGGTGACGATGACCTGCTCCCTTCGGAGAACAGGAGCTAGTCAACTCC 728
QY 364 GGCATCAAGTTCTACAGCGGTACGAATCGCTCAAGGAACATCGTTTCANTTCATCCGA 423
DB 729 GGCATCAAGTTCTACAGCGGTACGAATCGCTCAAGGAACATCGTTTCANTTCATCCGA 788
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QY 484 ACCAGCTGAAGATCTCTGCTGCGCAGCCCGGCAATGTCGCGCAAGATCGAGTGGTC 543
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QY 544 ATTTCCGAGGCGAGCTCATCAACAACACTCTCGACCCAGGCACTCTGCACTGTCTCGAA 603
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DB 1209 AAAAGTATTAAGGCAATGTCAGGTAAACCGCTCCGCGCCGACCCAGGCGTCCGCTAC 1268
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QY 1084 CCGCTATCTACACGACCGTGGAGATATCACCCAGACAGATGATTCCTGCTGTGG 1143
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QY 1264 GCTTTGGGAGATGACCCGGATAGCTTTGTAGGGGGTGTAGCTTTGTAGATCTGGG 1323
DB 1629 GCTTTGGGAGATGACCCGGATAGCTTTGTAGGGGGTGTAGCTTTGTAGATCTGGG 1688
QY 1324 GGTATTTGGGCGGAGTGTGTTTGTAG 1350
DB 1689 GGTATTTGGGCGGAGTGTGTTTGTAG 1715

US-07-923-724-7
; Sequence 7, Application US/07923724
; Patent No. 5780292
; GENERAL INFORMATION:
; APPLICANT: Nevalainen, Helena K.M.
; APPLICANT: Paloheimo, Maria T.
; APPLICANT: Mettinen-Oinonen, Arja S.K.
; APPLICANT: Torkkeli, Tuula K.
; APPLICANT: Cantrell, Michael
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Rambosek, John A.
; APPLICANT: Turunen, Marja K.
; APPLICANT: Egerstr m, Richard B.
; TITLE OF INVENTION: Production of Phytase Degrading Enzymes
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/923.724
; FILING DATE: 31-JUL-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/496,155
; FILING DATE: 19-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/044,077
; FILING DATE: 29-APR-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: UK 8610600
; FILING DATE: 30-APR-1986
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimbala, Michele A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 1050.0240004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2363 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: both
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(404..447, 550..1906)
; US-07-923-724-7
Query Match 94.4%; Score 1275; DB 1; Length 2363;
Best Local Similarity 96.7%; Pred. No. 0;
Matches 1302; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
QY 4 CTGGCAGTCCCGCTCCAGAAATCAATCCAGTTCCGATACGTCGATCAGGGGTATCAA 63
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DB 623 TGCTTCTCCGAGACTTCGCATCTTTGGGGTCAATACGACCGTTCTCTCTCTCGCAAAC 682
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Qy 244 GAGGAGATCCAGCAGAACCGACCACTTTTACGCGAAATATGCTTCTTGAAGACATAC 303
Db 803 GAGGAGATCCAGCAGAACCGACCACTTTTATGGAATATGCTTCTTGAAGACATAC 862
Qy 304 AACTACAGCTTGGGTGAGATGACTGACTCCCTTCGAGAACAGGAGTACTCAATCC 363
Db 863 AACTACAGCTTGGGTGAGATGACTGACTCCCTTCGAGAACAGGAGTACTCAATCC 922
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Db 923 GGCATCAAGTTCTACACGCGTACGATCGCTCAAGGACATCGTTCCATTCATCCGA 982
Qy 424 TCCTCTGGCTCCAGCGCGTATCATCAACCACTCTCGACCCAGGACCTGCTCTTCGAA 483
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Qy 484 ACCAAGCTGAAGGATCTCGTCCGACGCGCCCAATCGTCCGCAAGATCGAGTGGTC 543
Db 1043 ACCAAGCTGAAGGATCTCGTCCGACGCGCCCAATCGTCCGCAAGATCGAGTGGTC 1102
Qy 544 ATTTCCGAGGCGAGTCAATCAACCACTCTCGACCCAGGACCTGCTCTTCGAA 603
Db 1103 ATTTCCGAGGCGAGTCAATCAACCACTCTCGACCCAGGACCTGCTCTTCGAA 1162
Qy 604 GACAGCAATTTGGCGGATACCGTGAAGCAATTTACCGGACGCTTCCGCTCCAT 663
Db 1163 GACAGCAATTTGGCGGATACCGTGAAGCAATTTACCGGACGCTTCCGCTCCAT 1222
Qy 664 CGTCAACGCTGAGAGAACGCTCTCGGTGTGACTCTCACAGACAGAGTGAACCTAC 723
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Db 1283 CTATGACATGTCTCTTCGACACCATCTCCACGACACCGTTCGACCAAGCTGTC 1342
Qy 784 CCCTTCTGACCTGTTACCCATGAGGATGATCACTACGATCACTCCGCTCCGCTTG 843
Db 1343 CCCTTCTGACCTGTTACCCATGAGGATGATCACTACGATCACTCCGCTCCGCTTG 1402
Qy 844 AAAAAGTATTACGGCCATGTGACGTAACCGCTCGGCGCCGACCCAGGCGTCCGCTAC 903
Db 1403 AAAAATACTACGCCATGGCGAGGTAAACCGCTCGGCGCCGACCCAGGCGTCCGCTAC 1462
Qy 904 GCTAACGAGCTATCGCGCGTCTGACCACTCGGCTGTCCAGATGACAGTTCACAC 963
Db 1463 GCTAACGAGCTATCGCGCGTCTGACCACTCGGCTGTCCAGATGACAGTTCACAC 1522
Qy 964 CACACTTGGACTCGAGCGCGTCACTTTCCGCTCAACTCTACTCTCTACGGGACTTT 1023
Db 1523 CACACTTGGACTCGAGCGCGTCACTTTCCGCTCAACTCTACTCTCTACGGGACTTT 1082
Qy 1024 TCGCATGACAGGCAATCATCTCTCTCTTTGCTTTAGTCTGTGTAACAGGCACTAAG 1083
Db 1583 TCCACGATACGCGCATCATCTCTCTCTTTGCTTTGGTCTGTACACGCGCACTAAG 1642
Qy 1084 CCGTATCTACACGCGTGGAGATATACCCAGACAGATGATGATCTCGTCTGCTTGG 1143
Db 1643 CCGTATCTACACGCGTGGAGATATACCCAGACAGATGATGATGATCTCGTCTGCTTGG 1702
Qy 1144 ACGGTTCCGTTTGGTTCGCGTTTACGTCGAGATGATGAGTGTACGGGCGGAGCGAG 1203
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Qy 1204 CCGTGTGCTGCTGTTGTTAATGATCGGTTTCCGCTGCATGAGTGTCCGTTGAT 1263
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Qy 1264 GCTTTGGGAGATGTACCCGGATACCTTTTGTGAGGGGTTGAGCTTTCTAGATCTGG 1323
Db 1823 GCTTTGGGAGATGTACCCGGATACCTTTTGTGAGGGGTTGAGCTTTCTAGATCTGG 1882
Qy 1324 GGTGATTGGCGGAGTGTTTTGCTTAG 1350
Db 1883 GGTGATTGGCGGAGTGTTCGCTTAG 1909

RESULT 10

US-08-609-426A-7
; Sequence 7, Application US/08609426A
; Patent No. 5830733
; GENERAL INFORMATION:
; APPLICANT: Nevalainen, Helena K.M.
; APPLICANT: Paloheimo, Marja T.
; APPLICANT: Miettinen-Oinonen, Arja S.K.
; APPLICANT: Torkkeli, Tuula K.
; APPLICANT: Cantrell, Michael
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Rambosek, John A.
; APPLICANT: Turunen, Marja K.
; APPLICANT: Fagerstr m, Richard B.
; APPLICANT: Houston, Christine S.
; TITLE OF INVENTION: Production of Phytase Degrading Enzymes
; NUMBER OF INVENTION: in Trichoderma
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,426A
; FILING DATE: 01-MAR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/923,724
; FILING DATE: 31-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/496,155
; FILING DATE: 19-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/044,077
; FILING DATE: 29-APR-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: UK 8610600
; FILING DATE: 30-APR-1986
; ATTORNEY/AGENT INFORMATION:
; NAME: Reed, Grant E.
; REGISTRATION NUMBER: P-41,264
; REFERENCE/DOCKET NUMBER: 1050.0080001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2363 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: both
; FEATURE:
; NAME/KEY: CDS
; LOCATION: Join(404..447, 550..1906)
US-08-609-426A-7

Query Match 94.4%; Score 1275; DB 2; Length 2363;
Best Local Similarity 96.7%; Pred. No. 0;
Matches 1302; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 4 CTGGCAGTCCCGCTCGAGAAATCAATCCAGTTCGATACGGTCGATCAGGGGTATCAA 63
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DB GCTTTGGGAGATGTACCGGATAGCTTTGTGAGGGGTTGAGCTTTGCTAGATCTGGG 1882
QY 1324 GGTGATTGGCGGAGTGTTCCTTAG 1350
DB GGTGATTGGCGGAGTGTTCCTTAG 1909

RESULT 11
US-08-374-652C-1
; Sequence 1, Application US/08374652C
; Patent No. 5834286
; GENERAL INFORMATION:
; APPLICANT: NEVALAINEN, HELENA K.M.
; APPLICANT: PALOHEIMO, MARJA T.
; APPLICANT: FAGERSTROM, RICHARD B.
; APPLICANT: MIETTINEN-OINONEN, ARJA S.
; APPLICANT: TURUNEN, MARJA K.
; APPLICANT: RAMBOSK, JOHN A.
; APPLICANT: PIDDINGTON, CHRISTOPHER S.
; APPLICANT: HOUSTON, CHRISTINE S.
; APPLICANT: CANRELL, MICHAEL A.
; TITLE OF INVENTION: RECOMBINANT CELLS, DNA CONSTRUCTS, PHYTATE DEGRADING
; TITLE OF INVENTION: VECTORS AND METHODS FOR EXPRESSING
; TITLE OF INVENTION: ENZYMES IN DESIRED RATIOS
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/374,652C
; FILING DATE: 24-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07058
; FILING DATE: 27-JUL-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/925,401
; FILING DATE: 31-JUL-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: REED, GRANT E.
; REGISTRATION NUMBER: 41,264
; REFERENCE/DOCKET NUMBER: 1050.071001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600

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;
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2379 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(404..447, 550..1906)
; US-08-374-652C-1

Query Match          94.4%; Score 1275; DB 2; Length 2379;
Best Local Similarity 96.7%; Pred. No. 0;
Matches 1302; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

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Db 879 AACTACAGCTTGGGTGAGATGACTGACTCCCTTCGAGAGAACAGGAGCTAGTCACTCC 938
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Db 999 TCCTCTGGCTCCAGCCGCGTATCGCTCCGCGCAAGAAATTCATCGAGGCTTCCAGAGC 1058
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Db 1059 ACCAAGCTGAGGATCCCTCGTCCCGACCGCGGCAATCGTCGCCCAAGATCGAGTGGTC 1118
QY 544 ATTTCCGAGGCCAGCTCATCCAAACAACACTCTCGACCCAGGCACCTGCACTGTCTTCGAA 603
Db 1119 ATTTCCGAGGCCAGCTCATCCAAACAACACTCTCGACCCAGGCACCTGCACTGTCTTCGAA 1178
QY 604 GACAGCAATTTGGCGGATACCGTGAAGCCAAATTTCAACCGCAGTTCGTCCTCCATT 663
Db 1179 GACAGCAATTTGGCGGATACCGTGAAGCCAAATTTCAACCGCAGTTCGTCCTCCATT 1238
QY 664 CGTCAACGCTCGGAGAACGACTCTGCGGTGTGACTCTCAAGACACAGAGTGAACCTAC 723
Db 1239 CGTCAACGCTCGGAGAACGACTCTGCGGTGTGACTCTCAAGACACAGAGTGAACCTAC 1298
QY 724 CTCATGAGCATGTGCTCCTTCGACACCATCTCCACGACCGTTCGACACCAAGCTCTCC 783
Db 1299 CTCATGAGCATGTGCTCCTTCGACACCATCTCCACGACCGTTCGACACCAAGCTCTCC 1358
QY 784 CCCTTCTGTGACCTGTTCCACCATGACGAATGGATCAACTACGACTACCTCCAGTCCCTG 843
Db 1359 CCCTTCTGTGACCTGTTCCACCATGACGAATGGATCAACTACGACTACCTCCAGTCCCTG 1418
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QY 844 AAAAGTATTACGGCCATGTTGAGTAACCGCTCGGCCCGACGAGGGCGTTCGGCTAC 903
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QY 904 GTTAACGAGCTCATCGCCGTTGTGACCCACTCGCTGTCCAGATGACACCAAGTTCACAA 963
Db 1479 GTTAACGAGCTCATCGCCGTTGTGACCCACTCGCTGTCCAGATGACACCAAGTTCACAA 1538
QY 964 CACACTTTCGAGCTCGAGCCCGCTACCTTTCGCTCAACTCTACTCTCTACGGGACTTT 1023
Db 1539 CACACTTTCGAGCTCGAGCCCGCTACCTTTCGCTCAACTCTACTCTCTCTACGGGACTTT 1598
QY 1024 TCGCATGACACGCGCATCATCTCCATTTCTTTTGTCTTTAGTCTCTTACAAAGGCTACAG 1083
Db 1599 TCGCATGACACGCGCATCATCTCTATCTCTTTTGTCTTTTGGTCTCTGTACAAAGGCTACAG 1658
QY 1084 CGCTATCTACACGACCGTGGAGATATATCACCCAGACAGATGAGATTCTCGTCTCGTTGG 1143
Db 1659 CGCTATCTACACGACCGTGGAGATATATCACCCAGACAGATGAGATTCTCGTCTCGTTGG 1718
QY 1144 ACGGTTCCGTTTGGCTTTCGGGTTTGTACGTCGAGATGATGACGTGTTCAGGCGGAGCAGGAG 1203
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QY 1204 CGCTGGTCCGTTGCTTGGTTAATGATCGGTTTCCCGCTGCATGGGTTCCGGTTGAT 1263
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QY 1264 GCTTTGGGAGATGATACCCGGGATAGCTTTGTGAGGGGTTGAGCTTTGCTAGATCTGGG 1323
Db 1839 GCTTTGGGAGATGATACCCGGGATAGCTTTGTGAGGGGTTGAGCTTTGCTAGATCTGGG 1898
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Db 1899 GGTGATTGGCGGAGTGTGTTTTCCTTAG 1925

RESULT 12
US-09-155-855-5
; Sequence 5, Application US/09155855
; Patent No. 6139902
; GENERAL INFORMATION:
; APPLICANT: KONDO, Hidemasa
; APPLICANT: ANAZAWA, Hideharu
; APPLICANT: KANEKO, Syunichi
; APPLICANT: NAGASHIMA, Tadashi
; APPLICANT: TANGE, Tatsuya
; TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
; FILE REFERENCE: 81356/124
; CURRENT APPLICATION NUMBER: US/09/155,855
; EARLIER FILING DATE: 1998-10-05
; EARLIER APPLICATION NUMBER: WO PCT/JP97/01175
; EARLIER FILING DATE: 1997-04-04
; EARLIER APPLICATION NUMBER: JP 084314
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Aspergillus niger
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (1)..(45)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(45)
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (157)..(183)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (184)..(1512)
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FEATURE:
; NAME/KEY: CDS
; LOCATION: (157)..(1512)
US-09-155-855-5

Query Match
Best Local Similarity 87.6%; Score 1182.2; DB 3; Length 1515;
; Pred. No. 2.5e-301;
Matches 1244; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

QY 4 CTGGCAGTCCCGCTCGAGAAATCAATCCAGTTCGATACGGTCGATCAGGGGTATCAA 63
DB 169 CTGGCAGTCCCGCTCGAGAAATCAATCCAGTTCGATACGGTCGATCAGGGGTATCAA 228

QY 64 TGCCTTCGAGACTTCGATCTTGGGGTCAATACGCCAGTTCCTCTCTCGGCAAC 123
DB 229 TGCCTTCGAGACTTCGATCTTGGGGTCAATACGCCAGTTCCTCTCTCGGCAAC 288

QY 124 GAATCGGTATCTCCCTGAGGTGCGCGCGGATGCGAGTCACTTCGCTCAGGTCTTC 183
DB 289 AAATCGGCAATCTCCCTGATGTTCTCTCGCGGATGCCATGTCACTTCGCGCCAGGTCTC 348

QY 184 TCCGCTCATGGAGCGGTATCCGACCGACTCCAAGGCGAAGAAATATCTCCGCTCTCAT 243
DB 349 TCCGCTCATGGAGCGGTATCCGACCGACTCCAAGGCGAAGAAATATCTCCGCTCTCAT 408

QY 244 GAGGAGATCCAGCAAGACCGGACCACTTTGACGGAATAATATGCTTCCTGAAGACATAC 303
DB 409 GAGGAGATCCAGCAAGACCGGACCACTTCGAGGGGAAATATGCTTCCTGAAGACATAC 468

QY 304 AACTACAGTTCGGGTGAGATGACTGCTGCTCCGTCGAGAACAGGAGTAGTCAATCC 363
DB 469 AACTACAGTTCGGGTGAGATGACTGCTCCGTCGAGAACAGGAGTAGTCAATCC 528

QY 364 GGCATCAAGTTCACACGGTACGAATCGCTCAAGGAAACATCGTTCCATTCATCCGA 423
DB 529 GGCATCAAGTTCACACGGTACGAATCGCTCAAGGAAACATCGTTCCATTCATCCGA 588

QY 424 TCCTCGGCTCAGCGCGGTATGCTCCGCGAAGAAATATCTCGAGGGTTCAGAGC 483
DB 589 TCCTCGGCTCAGCGCGGTATGCTCCGCGAAGAAATATCTCGAGGGTTCAGAGC 648

QY 484 ACCAAGCTGAAGATTCCTCGTCCGAGCGCGGCAATCGTCCGCAAGATCGAGTGGTC 543
DB 649 ACTAAGCTGAAGATTCCTCGTCCGAGCGCGGCAATCGTCCGCAAGATCGAGTGGTC 708

QY 544 ATTTCCGAGGCGAGTCAATCAAAACACTCTCGACCCAGGCACTGCACTGTTTCGAA 603
DB 709 ATTTCCGAGGCGAGTCAATCAAAACACTCTCGACCCAGGCACTGCACTGTTTCGAA 768

QY 604 GACAGCAATGGCGGATACCGTCCGAGCAATTCACCGCACTTCGCTCCCTCCATT 663
DB 769 GATAGCAATGGCGGATACCGTCCGAGCAATTCACCGCACTTCGCTCCCTCCATT 828

QY 664 CGTCAACCTCTGGAGACGACTTCGCTGCTGCTCAAGACAGAGTCACTAC 723
DB 829 CGTCAACCTCTGGAGACGACTTCGCTGCTGCTCAAGACAGAGTCACTAC 888

QY 724 CTCATGGAGATGCTCTTCGACACCACTTCACCGACCGTCCGACCACTGCTCC 783
DB 889 CTCATGGAGATGCTCTTCGACACCACTTCACCGACCGTCCGACCACTGCTCC 948

QY 784 CCGTCTCTGACCTGTTCCACCATGACGAATGGATCAACTACGACTACCTCCAGTCTTG 843
DB 949 CCGTCTCTGACCTGTTCCACCATGACGAATGGATCAACTACGACTACCTCCAGTCTTG 1008

QY 844 AAAAGTATACGGCAATGTCAGGTAAACCGCTCGGCGCCGACCCAGGGGTCCGTAC 903
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QY 904 GCTAACGAGCTCATCGCCGCTCTGACCCACTCGGCTGTCCACGATGACACAGTTCACAC 963
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QY 964 CACACTTTGGACTCGAGCCCGCTACCTTTCCGCTCAACTCTCTACTCTCTACCGGACTTT 1023
DB 1129 CACACTTTGGACTCCAAACCGGCTACTTTCCGCTCAACTCTCTACTCTCTATCGGACTTT 1188

QY 1024 TGCATGACACGGCATCATCTCCATCTCTTTTGGTCTTTAGTCTGTACAAACGGGACTAAG 1083
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QY 1084 CGGCTATCTACACACCGCTGAGAAATATACCCAGACAGATGGATCTCGTCTCTTTGG 1143
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QY 1144 ACGGTTCCGTTTGGCTTCGCTTTGACGTCGAGATGATGACGAGTGTACGCGGAGCAGGAG 1203
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QY 1264 GCTTTGGGAGATGTACCCGGGATAGCTTTGTACGGGGTGTAGCTTTGTAGATCTGGG 1323
DB 1429 GCTTTGGGAGATGTACCCGGGATAGCTTCGTGAAAGGGTGTAGCTTTGTAGATCTGGG 1488

QY 1324 GGTGATTGGCGGAGTGTTCCTTAG 1350
DB 1489 GGTGATTGGCGGAGTGTTCCTTAG 1515

RESULT 13
US-09-543-744-5
; Sequence 5, Application US/09543744
; Patent No. 6309870
; GENERAL INFORMATION:
; APPLICANT: KONDO, Hidemasa
; APPLICANT: ANAZAWA, Hideharu
; APPLICANT: KANEKO, Syunichi
; APPLICANT: NAGASHIMA, Tadashi
; APPLICANT: TANGE, Tatsuya
; TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
; FILE REFERENCE: 81356/124
; CURRENT APPLICATION NUMBER: US/09/543,744
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 09/155,855
; PRIOR FILING DATE: 1998-10-05
; PRIOR APPLICATION NUMBER: JP 084314
; PRIOR FILING DATE: 1996-04-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Aspergillus niger
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (1)..(45)
; NAME/KEY: CDS
; LOCATION: (1)..(45)
; NAME/KEY: sig_peptide
; LOCATION: (157)..(183)
; NAME/KEY: mat_peptide
; LOCATION: (184)..(1512)
; NAME/KEY: CDS
; LOCATION: (157)..(1512)
US-09-543-744-5

Query Match 87.6%; Score 1182.2; DB 3; Length 1515;
Best Local Similarity 92.4%; Pred. No. 2.5e-301;
Matches 1244; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

QY 4 CTGGCAGTCCCGCTCGAGAAATCAATCCAGTTCGATACGGTCGATCAGGGGTATCAA 63
DB 169 CTGGCAGTCCCGCTCGAGAAATCAATCCAGTTCGATACGGTCGATCAGGGGTATCAA 228

QY 64 TGCTTCCGAGACTTCGATCTTTGGGTCATATGACGACCGTTCTTCTCTCTGGCAAC 123
Db 229 TGCTTCTCGAGACTTCGATCTTTGGGTCATATGACGACCGTTCTTCTCTGGCAAC 288
QY 124 GAATCGGTCTATCTCCCTGAGGTGCGCGCGGATGACAGTCACTTTCGTCAGGTCCTC 183
Db 289 AATCGGCAATCTCCCTGATGTTCTGCGGATGCATGTCACTTTCGCCAGGTTCTC 348
QY 184 TCCGTCATGAGCGCGGTATCCGACCGAATCAAGGGCAAGAAATACCTCCGTCCTCAT 243
Db 349 TCCGCCATGAGCAGCGTATCCGACCGAATCAAGGGCAAGAAATACCTCCGTCCTCAT 408
QY 244 GAGGAGATCCAGAGACGCGGACCGCTTTGACGGAATAATGCTTCTGGAAGACATAC 303
Db 409 GAGGAGATCCAGAGACGCGGACCGCTTTGAGGGGAATAATGCTTCTGGAAGACATAC 468
QY 304 AACTACAGCTTGGGTGAGATGACCTGACTCCCTTCGGAGAAACAGGAGTGTCAACTCC 363
Db 469 AACTACAGCTTGGGTCGGATGATCTGACTCCCTTCGGAGAGAGAGTGTCAACTCC 528
QY 364 GGCATCAAGTCTACGAGCGGTAGCATCGCTCACAGGAACATCGTTCCATTCATCCGA 423
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QY 424 TCCTCTGGCTCCAGCCGCGTATCGCTCCGCGCAAGAAATTCATCGAGGCTTCCAGAGC 483
Db 589 TCCTCAGGCTCCAGCCGCGTATCGCTCCGCGCAAGAAATTCATCGAGGCTTCCAGAGC 648
QY 484 ACCAAGCTGAAGGATCTCTGTCGCCAGCGCGGCAATCGTCCGCAAGATCGAGTGGTC 543
Db 649 ACTAAGCTGAAGGATCTCTGTCGCCAGCGCGGCAATCGTCCGCAAGATCGAGTGGTC 708
QY 544 ATTTCCGAGGCGAGCTCATCCAAACACTCTCCAGCCAGGCACTCTCACTGTCTTCGAA 603
Db 709 ATTTCCGAGGCGAGCAATCCAAACACTCTCGATCGGGCACTCTCACTGTCTTCGAA 768
QY 604 GACAGCAATTTGGCCGATACCGTCCGAAGCAATTTCCAGCCAGCTTCTGTCCTCCCTCAT 663
Db 769 GATAGCAATTTGGCCGATACCGTCCGAAGCAATTTCCAGCCAGCTTCTGTCCTCCCTCAT 828
QY 664 GGTCAAGCTCTGAGAGAGGCTCTCGGTGTGACTCTCACAGACAGAGTGCCTAC 723
Db 829 CGTCAAGCTCTGAGAGAGGCTCTCGGTGTGACTCTCACAGAGAGTGCCTAC 888
QY 724 CTATGAGACATGTCTCTTCGACACCATCTCCAGCAGCCGTCGACACCAAGTGTCC 783
Db 889 CTATGAGACATGTCTCTTCGACACCATCTCCAGCAGCCGTCGACACCAAGTGTCC 948
QY 784 CCCTTCTGTGACCTGTTCACCCATGACGAATGGATCAACTACGACTACCTCCAGTCTTG 843
Db 949 CCCTTCTGTGACCTGTTCACCCATGACGAATGGATCAACTACGACTACCTCCAGTCTTG 1008
QY 844 AAAAAGTATTACGCCATGTTGAGGTAAACCGCTCGGCCGACCCAGGGCGTCGGCTAC 903
Db 1009 AACAAATACTAGGCGCATGCGCAGGTAAACCGCTCGGCCGACCCAGGGCGTCGGCTAC 1068
QY 904 GCTAACGAGCTCATCGCCCGTCTGACCCACTTGGCTGTGACGATGACACAGTTCACAC 963
Db 1069 GCTAACGAGCTCATCGCCCGTCTGACCCACTTGGCTGTGACGATGACACAGTTCACAC 1128
QY 964 CACATTTGGACTCGAGCCCGGCTACCTTTCGCTCACTCACTCTCTACCGGACTTT 1023
Db 1129 CACATTTGGACTCGAGCCCGGCTACTTTCGCTCACTCACTCTCTACCGGACTTT 1188
QY 1024 TCGCATGACAAAGGATCATCTCATCTCTTTGCTTTAGTCTGTGACAGGCACTAAG 1083
Db 1189 TCGCATGACAAAGGATCATCTCATCTCTTTGCTTTGGTCTGTGACAGGCACTAAG 1248
QY 1084 CCGCTATCTACAGACCGTGGAGATATACCCAGACAGATGATCTGCTGCTTGG 1143
Db 1249 CCGCTGCTCTACAGACCGGAGATATACCCAGACCGATGAGTGTCTATCTGCTGG 1308

QY 1144 ACGGTTCCGTTTGTCTTCGCTTGTACGTCAGATGATGACAGTGTACGCGGAGCAGGAG 1203
Db 1309 ACGGTTCCGTTTGTCTTCGCTTGTACGTCAGATGATGACAGTGTACGCGGAGCAGGAG 1368
QY 1204 CCGTGTGTCGCTTGTCTTAAATGATCGCTTGTCCCGCTGCATGGGTGTCGGTTCAT 1263
Db 1369 CCGTGTGTCGCTTGTCTTAAATGATCGCTTGTTCGCTGCATGGGTGTCGGTTCAT 1428
QY 1264 GCTTTGGGAGATGTACCCGGATAGCTTTGTGAGGGGTTGAGCTTTGTAGATCTCGG 1323
Db 1429 GCTTTGGGAGATGTACCCGGATAGCTTTGTGAGGGGTTGAGCTTTGTAGATCTCGG 1488
QY 1324 GGTGATTGGCGGAGTGTTTGCTTTAG 1350
Db 1489 GGTGATTGGCGGAGTGTTCGCTTAG 1515

RESULT 14
US-09-929-060-5
; Sequence 5, Application US/09929060
; Patent No. 6548282
; GENERAL INFORMATION:
; APPLICANT: KONDO, HIDEWASA
; APPLICANT: ANAZAWA, HIDEHARU
; APPLICANT: KANEKO, SYUNICHI
; APPLICANT: NAGASHIMA, TADASHI
; APPLICANT: TANGE, TATSUYA
; TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
; FILE REFERENCE: 081356/0166
; CURRENT APPLICATION NUMBER: US/09/929,060
; CURRENT FILING DATE: 2001-08-05
; PRIOR APPLICATION NUMBER: 09/543,744
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 09/155,855
; PRIOR FILING DATE: 1998-10-05
; PRIOR APPLICATION NUMBER: JP 084314/1996
; PRIOR FILING DATE: 1996-04-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Aspergillus niger
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(45)
; NAME/KEY: CDS
; LOCATION: (157)..(1512)
US-09-929-060-5

Query Match 87.6%; Score 1182.2; DB 4; Length 1515;
Best Local Similarity 92.4%; Pred. No. 2.5e-301; Indels 0; Gaps 0;
Matches 1244; Conservative 0; Mismatches 103;

QY 4 CTGGCAGTCCCGCTTCGAGAAATCAATCCAGTTGCGATACGTCGATCAGGGGTATCAA 63
Db 169 CTGGCAGTCCCGCTTCGAGAAATCAATCCAGTTGCGATACGTCGATCAGGGGTATCAA 228
QY 64 TGCTTCTCGAGACTTCGATCTTTGGGTCATATGACGACCGTTCTCTCTGGCAAC 123
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QY 124 GAATCGGTCTATCTCCCTGAGGTGCGCGCGGATGACAGTCACTTTCGCTCAGGTCCTC 183
Db 289 AATCGGCAATCTCCCTGATGTTCTGCGGATGCCATGTCTCACTTTCGCCAGGTTCTC 348
QY 184 TCCGTCATGAGCGCGGTATCCGACCGAATCAAGGGCAAGAAATACCTCCGTCCTCAT 243
Db 349 TCCGCCATGAGCAGCGTATCCGACCGAATCAAGGGCAAGAAATACCTCCGTCCTCAT 408
QY 244 GAGGAGATCCAGAGACGCGGACCGCTTTGACGGAATAATGCTTCTGGAAGACATAC 303
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Qy	304	AAC	TACAGCTTTGGGTGCAGATGACTCTGATCCTCTTCGAGAAACAGGAGCTAGTCAACTCC	363
Db	469	AAC	TACAGCTTTGGGTGCAGATGATCTGATCTCCCTTCGAGAGCAGGAGCTGGTCAA	528
Qy	364	GCG	ATCAAGTTTCTACCAGCGTGAGAATTCGTCTCAAGAGAAACATCGTTCCAATTCA	423
Db	529	GCG	GTCAAGTTTCTACCAGCGATACGAATCGCTCACAGAAACATTGTCCCGTTCAT	588
Qy	424	TCCT	CTGGCTTCAGCGCGGTGATCGCCTTCGGGAGAAAATTCATCGAGGGCTTCAGAGC	483
Db	589	TCCT	CAGGCTTCAGCGCGGTGATTCCTCTCGGCAATAAATTCATCGAGGGCTTCAGAGC	648
Qy	484	ACCA	AGCTGAAGAGTCTCTCTGTCGCCAGCCGCGGCCAAATCGTCGCCCAAGATCGAGTGGTC	543
Db	649	ACTA	AGCTGAAGGATCTCTCTGTGCCAGCCGCGGCCAAATCGTCGCCCAAGATCGAGTGGTC	708
Qy	544	ATTT	CCGAGGCCAGCTCATCCAAACAACACTCTCGAACCCAGGCACTGCACTGCTCTTCGAA	603
Db	709	ATTT	CAGAGGCCAGCACATCCAAACAACACTCTCGATCCGGGCACTCGACOGTTTTTCGAA	768
Qy	604	GAC	AGCAATTTGGCCGATACCGTCEAAGCCAAATTTACCGCCACGTTCTGCCCTCCATT	663
Db	769	GAT	AGCAATTTGGCCGATGACATCGAAGCCAAATTTACCGCCACGTTCTGCCCTCCATT	828
Qy	664	CGT	CAACGCTCTGGAGAGGACCTCTCGGTGTGACTCTCACAGACACAGAAGTCACCTAC	723
Db	829	CGT	CAACGCTCTGGAGAGGACCTCTCTGGGGTGTCTCTCACGGACACAGAAGTAGCCTAC	888
Qy	724	CTCA	TGACATGTCTCTTCGACACCATCTCCAACCAAGCCGTCGACACCAAGCTGTCC	783
Db	889	CTCA	TGACATGTCTCTTCGACACCATCTCCAACCAAGCCGTCGACACCAAGCTGTCC	948
Qy	784	CCCT	CTGTGACCTGTTACCCATGACGATGGATCAACTACGATFACCTCCAGTCCCTG	843
Db	949	CCCT	CTGTGACCTGTTACCCATGAGAAATGGATCAACTACGATFACCTCCAGTCCCTG	1008
Qy	844	AAAA	GTATTACGCCCATGTGTGACAGGTAAACCCGCTCGGCCCGGACCCAGGGCGTCGGCTAC	903
Db	1009	AACAA	TACTACGGCCATGGCGCAGGTAAACCCGCTCGGCCCGGACCCAGGGCGTCGGCTAC	1068
Qy	904	GCTA	ACAGCTCATCGCCGCTGTGACCCATCGCCCTGTCCACGNATGACACGATTCCAAC	963
Db	1069	GCTA	ACAGCTCATCGCCGCTGTGACCCATCGCCCTGTCCACGNATGACACGATTCCAAC	1128
Qy	964	CACA	CTTTGGACGACCGCGGTACTCTTCCGCTCAACTCTACTCTCTACGGGACTTT	1023
Db	1129	CACA	CTTTGGACTCCAACCGCGGTACTCTTCCGCTCAACTCTCTCTATGGGACTTT	1188
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Qy	1144	ACGG	TTCCGTTTCTCGCTGTTGTACGTCGAGATGATCAGGTGTCAGGCGGAGCAGGAG	1203
Db	1309	ACGG	TTTCTTTGGGTCGCGCATGTACGTCGAGATGATGCAATGCAATGCCNGTCCGAGCAGGAG	1368
Qy	1204	CCGC	TGTCGCTGTTTGGTTAATGATFCGCGTTGTCCCCTGTCATGGGTCTCCGGTTGAT	1263
Db	1369	CCTT	TGTCGCTGTTTGGTTAATGATFCGCTGTGTTTCCGCTGTCATGGGTCTCCGGTTGAT	1428
Qy	1264	GCTT	TGGGAGATGTACCCGSGATGCTTTGTGAGGGGGTTGAGCTTTGCTACATCTGG	1323
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Qy	1324	GFTG	ATGGCGAGTGTTTTGCTTAG	1350
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RESULT 15
US-09-155-855-4
; Sequence 4, Application US/09155855
; Patent NO. 6139902
; GENERAL INFORMATION:
; APPLICANT: KONDO, Hidemasa
; APPLICANT: ANAZAWA, Hideharu
; APPLICANT: KANEKO, Syunichi
; APPLICANT: NAGASHIMA, Tadashi
; APPLICANT: TANGE, Tatsuya
; TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
; FILE REFERENCE: 81356/124
; CURRENT APPLICATION NUMBER: US/09/155,855
; CURRENT FILING DATE: 1998-10-05
; EARLIER APPLICATION NUMBER: WO PCT/JP97/01175
; EARLIER FILING DATE: 1997-04-04
; EARLIER APPLICATION NUMBER: JP 084314
; EARLIER FILING DATE: 1996-04-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1332
; TYPE: DNA
; ORGANISM: Aspergillus niger
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1332)
US-09-155-855-4

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Query Match 86.5%; Score 1167.2; DB 3; Length 1332
Best Local Similarity 92.3%; Pred. No. 2.1e-297;
Matches 1229; Conservative 0; Mismatches 103; Indels 0;

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121	Db	CCTGATGTTCTGCGGATGCCATGTACATTTGCCCGAGGTTCTCTCCCGCCATGGAGCA	180
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181	Db	CGGTATTCGACCGACTCCAAGGGCAAGAAATATCTCCGCTCTCATTCAGGAGAGATCCAGCAG	240
259	QY	AACGGCAGCACCTTTGACGGGAAATATGCGCTTCTGGAAGACATACAACTACACGCTTGGGT	318
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319	QY	GCAGATGACCTGCACTCCCTTCGGAGAACAGGAGCTAGTCAACTCCGGGCATCAAGTTCTTAC	378
301	Db	GGGATGATCTGACTCTCCCTTCGGAGACAGGAGCTGGTCAACTCCGGCGTCAAGTTCTTAC	360
379	QY	CAGCGGTACGAATCGCTCACAGGAACATCTGTTCCATTATCCGATGCTCTTGCTCCACG	438
361	Db	CAGCGATACGAATCGCTCACAGGAACATTTGTCCCGTTTCAATCCGATCTCCAGGCTCCAGC	420
439	QY	CGCGTGATCGGCTCCGCGCAGAAATTCATCAGGGCTTCCAGAGCACCAGCTGAGGAT	498
421	Db	CGCGTGATGTCCTCTGGCAATAAATTATCGAGGGCTTCCAGAGCCTTAGCTGAGGAT	480
499	QY	CTCTGTGCCAGCCCGGCCAATCGTCCGCCCAAGATCGAAGTGTCTATTTCCAGAGGCCAGC	558
481	Db	CCTCGTGCCAGCCCGGCCAATCGTCCGCCCAAGATCGAAGTGTCTATTTCCAGAGGCCAGC	540
559	QY	TCATCCAAACAACATCTTCGACCCAGGCACTGTGCACTGCTTTCGAGAGACAGCAATTTGGCC	618
541	Db	ACATCCAAACAACATCTTCGATCCGGGCACTGCAACCGTTTTCGAAGATACCAATTTGGCC	600

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Job time : 136 secs

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Total number of hits satisfying chosen parameters: 7280484

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Maximum Match 100%
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ALIGNMENTS

RESULT 1
US-10-079-709-33
; Sequence 33, Application US/10079709
; Publication No. US20030119163A1
; GENERAL INFORMATION:
; APPLICANT: Robert F.M. Van Gorcom
; APPLICANT: Willem Van Hartingsveldt
; APPLICANT: Petrus A. Van Paridon
; APPLICANT: Annemarie E. Veenstra
; APPLICANT: Rudolf G.M. Luttin
; APPLICANT: Gerardus Seiten
; TITLE OF INVENTION: Cloning and Expression of Microbial
; TITLE OF INVENTION: Phytase
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025-3471
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/079,709
; FILING DATE: 02-FEB-2002
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/233,510
; FILING DATE: 20-JAN-1999
; APPLICATION NUMBER: 07/688,578

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	ID	Description
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4	1345.4	99.7	2665	17	US-10-662-914-5
5	1345.4	99.7	2665	17	US-10-662-914-7
6	1345.4	99.7	2665	17	US-10-662-914-11
7	1345.4	99.7	2665	17	US-10-662-914-17
8	1345.4	99.7	2665	17	US-10-662-914-19
9	1345.4	99.7	2665	17	US-10-662-914-21
10	1345.4	99.7	2665	17	US-10-662-914-23
11	1345.4	99.7	2665	17	US-10-662-914-25
12	1345.4	99.7	2665	17	US-10-662-914-27

Sequence 29, Appl
Sequence 33, Appl
Sequence 15, Appl
Sequence 31, Appl
Sequence 35, Appl
Sequence 39, Appl
Sequence 41, Appl
Sequence 66, Appl
Sequence 37, Appl
Sequence 43, Appl
Sequence 45, Appl
Sequence 49, Appl
Sequence 51, Appl
Sequence 47, Appl
Sequence 53, Appl
Sequence 55, Appl
Sequence 5, Appl
Sequence 4, Appl
Sequence 168, App
Sequence 13, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 162, App
Sequence 3, Appl
Sequence 117, App
Sequence 140, App
Sequence 164, App
Sequence 166, App
Sequence 23, Appl
Sequence 22, Appl
Sequence 3, Appl
Sequence 10, Appl
Sequence 10, Appl

FILING DATE: 24-MAY-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Muraehige, Kate H.
 REGISTRATION NUMBER: 29,959
 REFERENCE/DOCKET NUMBER: 24615-20026.00
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-327-7250
 TELEFAX: 415-327-2951
 INFORMATION FOR SEQ ID NO: 33:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1404 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORGANISM: Aspergillus ficuum (Aspergillus niger)
 STRAIN: NRRL 3135
 US-10-079-709-33

Query Match 99.8%; Score 1347; DB 15; Length 1404;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4 CTGGCAGTCCCGCCTCGAGAAATCAATCCAGATTGCGATCGGTGCGATCAGGGGTATCAA 63
 58 CTGGCAGTCCCGCCTCGAGAAATCAATCCAGATTGCGATCGGTGCGATCAGGGGTATCAA 117
 64 TGCTTCTCGAGACTTCGCATCTTTGGGGTCAATACGACACCGTTCTCTCTGGCAAC 123
 118 TGCTTCTCGAGACTTCGCATCTTTGGGGTCAATACGACACCGTTCTCTCTGGCAAC 177
 124 GAATCGGTTCATCTCCCTGAGGTGCGCGCGGATGCGAGTCACTTTTCGTCAGGTCTC 183
 178 GAATCGGTTCATCTCCCTGAGGTGCGCGCGGATGCGAGTCACTTTTCGTCAGGTCTC 237
 184 TCCCGTTCATGAGGCGGTATCCGACCGACTTCAAGGGCAAGAAATATCTCCGCTCTCAT 243
 238 TCCCGTTCATGAGGCGGTATCCGACCGACTTCAAGGGCAAGAAATATCTCCGCTCTCAT 297
 244 GAGGAGATCCAGAGACGCGACACACTTTGACGGGAATATGCTTCTTCAAGACATAC 303
 298 GAGGAGATCCAGAGACGCGACACACTTTGACGGGAATATGCTTCTTCAAGACATAC 357
 304 AACTACAGCTTGGGTGAGATGACCTGACCTCCCTTCGAGAACAGGAGTGTCAACTCC 363
 358 AACTACAGCTTGGGTGAGATGACCTGACCTCCCTTCGAGAACAGGAGTGTCAACTCC 417
 364 GGCATCAAGTCTACAGCGGTAGGAATCGTCAAGGAACATCGTTTCATTCATCCGA 423
 418 GGCATCAAGTCTACAGCGGTAGGAATCGTCAAGGAACATCGTTTCATTCATCCGA 477
 424 TCCTCTGGCTCCAGCGGTGATCGCTCCGCAAGAAATTCATCGAGGCTTCCAGAGC 483
 478 TCCTCTGGCTCCAGCGGTGATCGCTCCGCAAGAAATTCATCGAGGCTTCCAGAGC 537
 484 ACCAAGCTGAAGATTCCTGTCGCGAGCGCGCAATTCGTCGCCAAGATCGACGTGGTC 543
 538 ACCAAGCTGAAGATTCCTGTCGCGAGCGCGCAATTCGTCGCCAAGATCGACGTGGTC 597
 544 ATTTCCGAGGCGAGTTCATCAACACACTCTCGACCCAGGACCTGCTGCTCGAA 603
 598 ATTTCCGAGGCGAGTTCATCAACACACTCTCGACCCAGGACCTGCTGCTCGAA 657
 604 GACAGGAATGCGCGATACCGTTCGAAGCAATTTTCCAGCCCAAGTTCGTCGCCCTCAT 663
 658 GACAGGAATGCGCGATACCGTTCGAAGCAATTTTCCAGCCCAAGTTCGTCGCCCTCAT 717
 664 CGTCAAGCTCTGAGACGACCTGTCGGGTGACTCTCACAGACACAGAGTGACCTTAC 723
 718 CGTCAAGCTCTGAGACGACCTGTCGGGTGACTCTCACAGACACAGAGTGACCTTAC 777

724 CTCATGGACATGTGCTCTTTCGACACCATCTCCACGACACCGTTCGACACCAAGTGTCC 783
 778 CTCATGGACATGTGCTCTTTCGACACCATCTCCACGACACCGTTCGACACCAAGTGTCC 837
 784 CCCTTCTGTGACTGTTTCCACCATGAGCAATGAGTCAACTAGACTACTCTCAGTCTTGG 843
 838 CCCTTCTGTGACTGTTTCCACCATGAGCAATGAGTCAACTAGACTACTCTCAGTCTTGG 897
 844 AAAAAGTATTAGCGCATGGTGCAGGTAAACCGCTCGGCCCGACCCAGGCGCTCGGCTAC 903
 898 AAAAAGTATTAGCGCATGGTGCAGGTAAACCGCTCGGCCCGACCCAGGCGCTCGGCTAC 957
 904 GCTAACGAGTCAATCGCCCGTCTGACCCACTCGCTCTCCAGTGAACACAGTTCGAAC 963
 958 GCTAACGAGTCAATCGCCCGTCTGACCCACTCGCTCTCCAGTGAACACAGTTCGAAC 1017
 964 CACACTTTGGACTCGAGCCCGCTACCTTTCCGCTCAACTCTACTCTCTACCGGACTTT 1023
 1018 CACACTTTGGACTCGAGCCCGCTACCTTTCCGCTCAACTCTACTCTCTACCGGACTTT 1077
 1024 TCGATGACACCGCATCACTCCATCTCTTTTGTAGTCTGTACAACGGCACTAAG 1083
 1078 TCGCATGACACCGCATCACTCTCTTTTGTAGTCTGTACAACGGCACTAAG 1137
 1084 CGGCTATCTACCAACCGGTGAGAAATATACCCAGACAGATGGATTCTCTCTGCTTGG 1143
 1138 CGGCTATCTACCAACCGGTGAGAAATATACCCAGACAGATGGATTCTCTCTGCTTGG 1197
 1144 ACGGTTTCGTTTCTTCGCTTGTACGTCGAGATGATGAGTTCAGGCGGAGCAGGAG 1203
 1198 ACGGTTTCGTTTCTTCGCTTGTACGTCGAGATGATGAGTTCAGGCGGAGCAGGAG 1257
 1204 CGGCTGCTCGGTCCTTGTAAATGATCGGTTGTCGCTGTCATGGGTGTCGGTTCGAT 1263
 1258 CGGCTGCTCGGTCCTTGTAAATGATCGGTTGTCGCTGTCATGGGTGTCGGTTCGAT 1317
 1264 GCTTTGGGAGATGATACCCGGGATAGCTTTTGTAGGGGGTTCAGCTTTGCTAGATCTGG 1323
 1318 GCTTTGGGAGATGATACCCGGGATAGCTTTTGTAGGGGGTTCAGCTTTGCTAGATCTGG 1377
 1324 GGTGATTGGGCGAGTGTTCCTTAG 1350
 1378 GGTGATTGGGCGAGTGTTCCTTAG 1404

RESULT 2

US-10-662-914-1
 ; Sequence 1, Application US/10662914
 ; Publication No. US20040126844A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lei, Xingen
 ; APPLICANT: Mullane, Edward J
 ; APPLICANT: Ullah, Abul H. J.
 ; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTAES
 ; FILE REFERENCE: 19603/4261
 ; CURRENT APPLICATION NUMBER: US/10/662,914
 ; PRIOR FILING DATE: 2003-09-15
 ; PRIOR APPLICATION NUMBER: 60/410,736
 ; PRIOR FILING DATE: 2002-09-13
 ; NUMBER OF SEQ ID NOS: 59
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 2665
 ; TYPE: DNA
 ; ORGANISM: Aspergillus niger
 US-10-662-914-1

Query Match 99.8%; Score 1347; DB 17; Length 2665;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 4 CTGGCAGTCCCGCCTCGAGAAATCAATCCAGTTGCGATCAGGTGCGATCAGGGGTATCAA 63

Db 842 CTGGCAGTCCCGCCCTCGAGAAATCAATCCAGTTGGATACGCTCGATCAGGGGTATCAA 901
QY 64 TGTCTCTCCGAGACTTCGCAATCTTTGGGGTCAATACGACCGGTTCTTCTCTCTGGCAAC 123
Db 902 TGTCTCTCCGAGACTTCGCAATCTTTGGGGTCAATACGACCGGTTCTTCTCTCTGGCAAC 961
QY 124 GAATCGGTATCTCCCTGAGGTGCGCGCGGATGAGAGTCACTTTCCGTCAGGTCCTC 183
Db 962 GAATCGGTATCTCCCTGAGGTGCGCGCGGATGAGAGTCACTTTCCGTCAGGTCCTC 1021
QY 184 TCCCGTCATGAGCGGGTATCCGACCGACTCCAAAGGCAAGAAATCACTCCCGTCTCAT 243
Db 1022 TCCCGTCATGAGCGGGTATCCGACCGACTCCAAAGGCAAGAAATCACTCCCGTCTCAT 1081
QY 244 GAGGAGATCCAGACAGACCGACCACTTTGACGGAATATGCTTCTCTGAGACATAC 303
Db 1082 GAGGAGATCCAGACAGACCGACCACTTTGACGGAATATGCTTCTCTGAGACATAC 1141
QY 304 AACTACAGCTTGGGTGAGATGACCTGACTCCCTTCGGAGAACAGAGCTAGTCAACTCC 363
Db 1142 AACTACAGCTTGGGTGAGATGACCTGACTCCCTTCGGAGAACAGAGCTAGTCAACTCC 1201
QY 364 GGATCAAGTTCTACAGCGGTAGCAATCGCTCAAGGAACATCGTTCATTCATCCGA 423
Db 1202 GGATCAAGTTCTACAGCGGTAGCAATCGCTCAAGGAACATCGTTCATTCATCCGA 1261
QY 424 TCCCTCGCTCCAGCGCGGTATCGCTCCGGAAGAAATTCATCGAGGGCTTCCAGAGC 483
Db 1262 TCCCTCGCTCCAGCGCGGTATCGCTCCGGAAGAAATTCATCGAGGGCTTCCAGAGC 1321
QY 484 ACCAAGCTGAAGGATCTCGTCCGACCGCGGCAATCGTCCGCAAGATCGAGTGGTC 543
Db 1322 ACCAAGCTGAAGGATCTCGTCCGACCGCGGCAATCGTCCGCAAGATCGAGTGGTC 1381
QY 544 ATTTCCGAGCGGCTATCCAAACACTCTGACCCAGCAGCTCAGTCTTCGAA 603
Db 1382 ATTTCCGAGCGGCTATCCAAACACTCTGACCCAGCAGCTCAGTCTTCGAA 1441
QY 604 GACAGCAATTTGGCGGATACCGTGAAGCCAAATTTACCGCAGCTTCGTCCTCCATT 663
Db 1442 GACAGCAATTTGGCGGATACCGTGAAGCCAAATTTACCGCAGCTTCGTCCTCCATT 1501
QY 664 CGTCAACGCTCGGAGAACGACTCGCGGTGATCTCTCACAGACAGAGTGAACCTAC 723
Db 1502 CGTCAACGCTCGGAGAACGACTCGCGGTGATCTCTCACAGACAGAGTGAACCTAC 1561
QY 724 CTCATGGACATGTCTCTTCGACACCATCTCCACCGACCGTCGACACCAAGCTCTCC 783
Db 1562 CTCATGGACATGTCTCTTCGACACCATCTCCACCGACCGTCGACACCAAGCTCTCC 1621
QY 784 CCCTTCTGTGACCTGTTCAACCATGACGAATGGATCACTACGACTACCTCCAGTCTTG 843
Db 1622 CCCTTCTGTGACCTGTTCAACCATGACGAATGGATCACTACGACTACCTCCAGTCTTG 1681
QY 844 AAAAAGTATTACGCCATGTTGCAAGTAAACCGCTCGSCCGGACCCAGGGGTCGGGTAC 903
Db 1682 AAAAAGTATTACGCCATGTTGCAAGTAAACCGCTCGSCCGGACCCAGGGGTCGGGTAC 1741
QY 904 GCTAACGAGCTCATGCGCGGTCTGACCCACTCGCCTGTCCACGATGACACAGTTCAAC 963
Db 1742 GCTAACGAGCTCATGCGCGGTCTGACCCACTCGCCTGTCCACGATGACACAGTTCAAC 1801
QY 964 CACATTTGGATCGAGCGCGGTACCTTTCGGCTCAACTCTACTCTACGCGGACTTT 1023
Db 1802 CACATTTGGATCGAGCGCGGTACCTTTCGGCTCAACTCTACTCTACGCGGACTTT 1861
QY 1024 TCGCATGACAGGGATATCTCCATTCTCTTTGTTTTAGTCTGTACACGGCACTAAG 1083
Db 1862 TCGCATGACAGGGATATCTCCATTCTCTTTGTTTTAGTCTGTACACGGCACTAAG 1921
QY 1084 CCGCTATCTPACCAACCGTGGAGAAATATACCCAGACAGATGGAATCTCGTCTGCTGG 1143

Db 1922 CCGCTATCTACCAACGACCGTGGAGAAATATACCCAGACAGATGGAATCTCGTCTGCTGG 1981
QY 1144 ACGGTTCCGTTTGTCTTCGCGTTTGTAGCTCGAGATGATGAGTGTACAGCGGACAGAG 1203
Db 1982 ACGGTTCCGTTTGTCTTCGCGTTTGTAGCTCGAGATGATGAGTGTACAGCGGACAGAG 2041
QY 1204 CCGCTGGTCCGTCCTTGGTTAATGATCGCGTTCGCGCTGCAATGGGTTCGCGTTGAT 1263
Db 2042 CCGCTGGTCCGTCCTTGGTTAATGATCGCGTTCGCGCTGCAATGGGTTCGCGTTGAT 2101
QY 1264 GCTTTGGGAGATGTACCCGGATAGCTTTGTAGGGGTTGAGCTTTGCTAGATCTGG 1323
Db 2102 GCTTTGGGAGATGTACCCGGATAGCTTTGTAGGGGTTGAGCTTTGCTAGATCTGG 2161
QY 1324 GGTGATTGGCGGAGTGTTCCTTGTAG 1350
Db 2162 GGTGATTGGCGGAGTGTTCCTTGTAG 2188

RESULT 3

US-10-079-709-31
; Sequence 31, Application US/10079709
; Publication No. US20030119163A1
; GENERAL INFORMATION:
; APPLICANT: Robert F.M. Van Gorcom
; APPLICANT: Willem Van Hartingsveldt
; APPLICANT: Petrus A. Van Faridon
; APPLICANT: Anemarie E. Veenstra
; APPLICANT: Rudolf G.M. Vuttin
; APPLICANT: Gerardus Selten
; TITLE OF INVENTION: Cloning and Expression of Microbial
; TITLE OF INVENTION: Phytase
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025-3471
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/079,709
; FILING DATE: 02-FEB-2002
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/233,510
; FILING DATE: 20-JAN-1999
; APPLICATION NUMBER: 07/688,578
; FILING DATE: 24-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20026.00
; TELEPHONE: 415-327-7250
; TELEFAX: 415-327-2951
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6756 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Aspergillus ficum (Aspergillus niger)

; TYPE: DNA									
; ORGANISM: Aspergillus niger									
US-10-662-914-5									
Query Match									
Best Local Similarity 99.7%; Score 1345.4; DB 17; Length 2665;									
Matches 1346; Conservative 0; Mismatches 1; Indels 0; Gaps 0;									
Qy	4	CTGGCAGTCCCGCTCGAGAAATCAATCCAGTTGGATACGGTTCGATCAGGGGTATCAA	63						
Db	842	CTGGCAGTCCCGCTCGAGAAATCAATCCAGTTGGATACGGTTCGATCAGGGGTATCAA	901						
Qy	64	TGCTTCTCCGAGATTCCGATCTTTGGGGTCAATPACACCGTTCTTCTCTCTGGCAAAAC	123						
Db	902	TGCTTCTCCGAGATTCCGATCTTTGGGGTCAATPACACCGTTCTTCTCTCTGGCAAAAC	961						
Qy	124	GAATCGGTATCTCCCTGAGGTGCCCGGGATGCGAGTCACTTTCGCTCAGGTCCCTC	183						
Db	962	GAATCGGTATCTCCCTGAGGTGCCCGGGATGCGAGTCACTTTCGCTCAGGTCCCTC	1021						
Qy	184	TCCCGTATGAGCGCGGTATCCGACCGGACTCCAGGGCAAGAAATACTCCCGCTCTCAT	243						
Db	1022	TCCCGTATGAGCGCGGTATCCGACCGGACTCCAGGGCAAGAAATACTCCCGCTCTCAT	1081						
Qy	244	GAGGAGATCCAGCAACCGGACCACTTTTGACGAAATATGCTTCTCTGAAGACATAC	303						
Db	1082	GAGGAGATCCAGCAACCGGACCACTTTTGACGAAATATGCTTCTCTGAAGACATAC	1141						
Qy	304	AACATACAGTTGGGTGAGATGACTGACTCCCTTCGGAGAACAGGAGTACCACTCC	363						
Db	1142	AACATACAGTTGGGTGAGATGACTGACTCCCTTCGGAGAACAGGAGTACCACTCC	1201						
Qy	364	GGCATCAAGTTCTACCAAGCGGTACGAATCGTCTCAAGGAACATCGTTCCATTCAACGA	423						
Db	1202	GGCATCAAGTTCTACCAAGCGGTACGAATCGTCTCAAGGAACATCGTTCCATTCAACGA	1261						
Qy	424	TCCCTGGCTCCAGCGGTGATCGCTCCGGCAAGAAATCATCGAGGCTTCCAGAGC	483						
Db	1262	TCCCTGGCTCCAGCGGTGATCGCTCCGGCAAGAAATCATCGAGGCTTCCAGAGC	1321						
Qy	484	ACCAAGCTGAAGGATCCTCGTCCCGAGCCCGGCAATTCGCGCAAGATCGAGTGGTC	543						
Db	1322	ACCAAGCTGAAGGATCCTCGTCCCGAGCCCGGCAATTCGCGCAAGATCGAGTGGTC	1381						
Qy	544	ATTTCCGAGGCGAGTCAATCAA CAACACTCTGACCCAGGACCTGCTCTTCGAA	603						
Db	1382	ATTTCCGAGGCGAGTCAATCAA CAACACTCTGACCCAGGACCTGCTCTTCGAA	1441						
Qy	604	GACAGCAATTTGGCCGATACCGTCAAGCCCAATTTCAACCGCACTGCTCCCTCCATT	663						
Db	1442	GACAGCAATTTGGCCGATACCGTCAAGCCCAATTTCAACCGCACTGCTCCCTCCATT	1501						
Qy	664	CGTCAACGCTCGAGAACGACCTGTCCGGTGTGACTCTTCACAGACACAGAAAGTGA	723						
Db	1502	CGTCAACGCTCGAGAACGACCTGTCCGGTGTGACTCTTCACAGACACAGAAAGTGA	1561						
Qy	724	CTCATGACATGTCTCTCGACACCATCTCCAGCAGCAGCCGTCGACACCAAGCTGTC	783						
Db	1562	CTCATGACATGTCTCTCGACACCATCTCCAGCAGCAGCCGTCGACACCAAGCTGTC	1621						
Qy	784	CCCTTCTGTGACCTGTTCAACCCATGACGAATGGAATCACTACGACTACCTCCAGTCC	843						
Db	1622	CCCTTCTGTGACCTGTTCAACCCATGACGAATGGAATCACTACGACTACCTCCAGTCC	1681						
Qy	844	AAAAAGTATTACGGCCATGTGTGAGGTAAACCCGCTCGGCCCGACCCAGGGGTCCGTAC	903						
Db	1682	AAAAAGTATTACGGCCATGTGTGAGGTAAACCCGCTCGGCCCGACCCAGGGGTCCGTAC	1741						
Qy	904	GCTAACGAGCTCATCGCCCGTCTGACCCACTCGCTGTCCACGATGACACAGTTCACAC	963						
Db	1742	GCTAACGAGCTCATCGCCCGTCTGACCCACTCGCTGTCCACGATGACACAGTTCACAC	1801						
Qy	964	CACACTTTGAGACTCGAGCCCGGCTACCTTTCCGCTCAACTCTCTCTACGCGGACTTT	1023						
RESULT 5									
US-10-662-914-7									
; Sequence 7, Application US/10662914									
; Publication No. US20040126844A1									
; GENERAL INFORMATION:									
; APPLICANT: Lei, Xingren									
; APPLICANT: Mullaney, Edward J									
; APPLICANT: Ullah, Abul H.J.									
; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTASES									
; FILE REFERENCE: 19603/4261									
; CURRENT APPLICATION NUMBER: US/10/662,914									
; CURRENT FILING DATE: 2003-09-15									
; PRIOR APPLICATION NUMBER: 60/410,736									
; PRIOR FILING DATE: 2002-09-13									
; NUMBER OF SEQ ID NOS: 69									
; SOFTWARE: PatentIn Ver. 2.1									
; SEQ ID NO 7									
; LENGTH: 2665									
; TYPE: DNA									
; ORGANISM: Aspergillus niger									
US-10-662-914-7									
Query Match									
Best Local Similarity 99.7%; Score 1345.4; DB 17; Length 2665;									
Matches 1346; Conservative 0; Mismatches 1; Indels 0; Gaps 0;									
Qy	4	CTGGCAGTCCCGCTCGAGAAATCAATCCAGTTGGATACGGTTCGATCAGGGGTATCAA	63						
Db	842	CTGGCAGTCCCGCTCGAGAAATCAATCCAGTTGGATACGGTTCGATCAGGGGTATCAA	901						
Qy	64	TGCTTCTCCGAGATTCCGATCTTTGGGGTCAATPACACCGTTCTTCTCTCTGGCAAAAC	123						
Db	902	TGCTTCTCCGAGATTCCGATCTTTGGGGTCAATPACACCGTTCTTCTCTCTGGCAAAAC	961						
Qy	124	GAATCGGTATCTCCCTGAGGTGCCCGGGATGCGAGTCACTTTCGCTCAGGTCCCTC	183						
Db	962	GAATCGGTATCTCCCTGAGGTGCCCGGGATGCGAGTCACTTTCGCTCAGGTCCCTC	1021						
Qy	184	TCCCGTATGAGCGCGGTATCCGACCGGACTCCAGGGCAAGAAATACTCCCGCTCTCAT	243						
Db	1022	TCCCGTATGAGCGCGGTATCCGACCGGACTCCAGGGCAAGAAATACTCCCGCTCTCAT	1081						
Qy	244	GAGGAGATCCAGCAACCGGACCACTTTTGACGAAATATGCTTCTCTGAAGACATAC	303						
Db	1082	GAGGAGATCCAGCAACCGGACCACTTTTGACGAAATATGCTTCTCTGAAGACATAC	1141						
Qy	304	AACATACAGTTGGGTGAGATGACTGACTCCCTTCGGAGAACAGGAGTACCACTCC	363						
Db	1142	AACATACAGTTGGGTGAGATGACTGACTCCCTTCGGAGAACAGGAGTACCACTCC	1201						
Qy	364	GGCATCAAGTTCTACCAAGCGGTACGAATCGTCTCAAGGAACATCGTTCCATTCAACGA	423						
Db	1202	GGCATCAAGTTCTACCAAGCGGTACGAATCGTCTCAAGGAACATCGTTCCATTCAACGA	1261						
Qy	424	TCCCTGGCTCCAGCGGTGATCGCTCCGGCAAGAAATCATCGAGGCTTCCAGAGC	483						
Db	1262	TCCCTGGCTCCAGCGGTGATCGCTCCGGCAAGAAATCATCGAGGCTTCCAGAGC	1321						
Qy	484	ACCAAGCTGAAGGATCCTCGTCCCGAGCCCGGCAATTCGCGCAAGATCGAGTGGTC	543						
Db	1322	ACCAAGCTGAAGGATCCTCGTCCCGAGCCCGGCAATTCGCGCAAGATCGAGTGGTC	1381						
Qy	544	ATTTCCGAGGCGAGTCAATCAA CAACACTCTGACCCAGGACCTGCTCTTCGAA	603						
Db	1382	ATTTCCGAGGCGAGTCAATCAA CAACACTCTGACCCAGGACCTGCTCTTCGAA	1441						
Qy	604	GACAGCAATTTGGCCGATACCGTCAAGCCCAATTTCAACCGCACTGCTCCCTCCATT	663						
Db	1442	GACAGCAATTTGGCCGATACCGTCAAGCCCAATTTCAACCGCACTGCTCCCTCCATT	1501						
Qy	664	CGTCAACGCTCGAGAACGACCTGTCCGGTGTGACTCTTCACAGACACAGAAAGTGA	723						
Db	1502	CGTCAACGCTCGAGAACGACCTGTCCGGTGTGACTCTTCACAGACACAGAAAGTGA	1561						
Qy	724	CTCATGACATGTCTCTCGACACCATCTCCAGCAGCAGCCGTCGACACCAAGCTGTC	783						
Db	1562	CTCATGACATGTCTCTCGACACCATCTCCAGCAGCAGCCGTCGACACCAAGCTGTC	1621						
Qy	784	CCCTTCTGTGACCTGTTCAACCCATGACGAATGGAATCACTACGACTACCTCCAGTCC	843						
Db	1622	CCCTTCTGTGACCTGTTCAACCCATGACGAATGGAATCACTACGACTACCTCCAGTCC	1681						
Qy	844	AAAAAGTATTACGGCCATGTGTGAGGTAAACCCGCTCGGCCCGACCCAGGGGTCCGTAC	903						
Db	1682	AAAAAGTATTACGGCCATGTGTGAGGTAAACCCGCTCGGCCCGACCCAGGGGTCCGTAC	1741						
Qy	904	GCTAACGAGCTCATCGCCCGTCTGACCCACTCGCTGTCCACGATGACACAGTTCACAC	963						
Db	1742	GCTAACGAGCTCATCGCCCGTCTGACCCACTCGCTGTCCACGATGACACAGTTCACAC	1801						
Qy	964	CACACTTTGAGACTCGAGCCCGGCTACCTTTCCGCTCAACTCTCTCTACGCGGACTTT	1023						

304 AACTACAGCTTGGGTGCAGATGACCTGACTCCCTTCGGAGAACAGGAGCTAGTCAACTCC 363
1142 AACTACAGCTTGGGTGCAGATGACCTGACTCCCTTCGGAGAACAGGAGCTAGTCAACTCC 1201
364 GGCATCAAGTTCTACACAGCGGTACGAATCGGTTCACAAAGGAACATCGTTCCATTTCATCCGA 423
1202 GGCATCAAGTTCTACACAGCGGTACGAATCGGTTCACAAAGGAACATCGTTCCATTTCATCCGA 1261
424 TCCTCTGGCTCAGCGCGGTGATCCCTTCGGCAGAAATTCATCGAGGGCTTCAGAGC 483
1262 TCCTCTGGCTCAGCGCGGTGATCCCTTCGGCAGAAATTCATCGAGGGCTTCAGAGC 1321
484 ACCAAGCTGAAGGATCTCTGTCGCCAGCGCGCCCAATCGTCCGCAAGATCGAGTGGTC 543
1322 ACCAAGCTGAAGGATCTCTGTCGCCAGCGCGCCCAATCGTCCGCAAGATCGAGTGGTC 1381
544 ATTTCCGAGGCGAGCTCATCCAAACACATCTCGACCCAGGCACTGCACTGTCTTCGAA 603
1382 ATTTCCGAGGCGAGCTCATCCAAACACATCTCGACCCAGGCACTGCACTGTCTTCGAA 1441
604 GACAGCGAATTCGGCGATACCGTGCAGGCAATTTCCACGCCACGTTGCTCCCTCCATT 663
1442 GACAGCGAATTCGGCGATACCGTGCAGGCAATTTCCACGCCACGTTGCTCCCTCCATT 1501
664 GGTCAACGTCTGGAGACGACCTGTCGGGTGATCTCTCAGACACAGAGTGAACCTAC 723
1502 GGTCAACGTCTGGAGACGACCTGTCGGGTGATCTCTCAGACACAGAGTGAACCTAC 1561
724 CTCATGGACATGTGCTCTTCGACACCATCTCCACGACCGTTCGACACCAAGCTGCC 783
1562 CTCATGGACATGTGCTCTTCGACACCATCTCCACGACCGTTCGACACCAAGCTGCC 1621
784 CCTTCTGTGACCTGTTCAACCCATGACGAATGGATCAACTACGACTACCTCCAGTCCCTTG 843
1622 CCTTCTGTGACCTGTTCAACCCATGACGAATGGATCAACTACGACTACCTCCAGTCCCTTG 1681
844 AAAAGTATTAGGCGCATGTTGCGAGTAAACCGCTCCGCGCCGACCCAGGGCGTGGTAC 903
1682 GAAAGTATTAGGCGCATGTTGCGAGTAAACCGCTCCGCGCCGACCCAGGGCGTGGTAC 1741
904 GCTAACGAGCTCATCGCCGCTGTACCCACTCGCTGTCCACGATGACACCAAGTTCACAC 963
1742 GCTAACGAGCTCATCGCCGCTGTACCCACTCGCTGTCCACGATGACACCAAGTTCACAC 1801
964 CACACTTTGGACTCAGAGCCGGCTACCTTTCCGCTCAACTCTCTCTACGCGGACTTT 1023
1802 CACACTTTGGACTCAGAGCCGGCTACCTTTCCGCTCAACTCTCTCTACGCGGACTTT 1861
1024 TCGCATGACAAAGGATCATCTCATCTCTTTAGTCTGTGATCAACGCGCACTAAG 1083
1862 TCGCATGACAAAGGATCATCTCATCTCTTTAGTCTGTGATCAACGCGCACTAAG 1921
1084 CCGCTATCTACACGACCGTGGAGAAATACCCAGACAGATGGAATCTCGTCTGTGTTG 1143
1922 CCGCTATCTACACGACCGTGGAGAAATACCCAGACAGATGGAATCTCGTCTGTGTTG 1981
1144 ACGGTCGCTTTGCTTCGCTTTGCTACGTCAGATGATGATGTCAGGCGGAGCAGGAG 1203
1982 ACGGTCGCTTTGCTTCGCTTTGCTACGTCAGATGATGATGTCAGGCGGAGCAGGAG 2041
1204 CCGTGTGTCGCTGCTTTGTTAATGATCGGCTGTCGCCGTCGATGGGTGTCGGGTTGAT 1263
2042 CCGTGTGTCGCTGCTTTGTTAATGATCGGCTGTCGCCGTCGATGGGTGTCGGGTTGAT 2101
1264 GCTTTGGGAGATGATCCCGGGATAGCTTTGTGAGGGGGTTGAGCTTTGCTAGATCTGGG 1323
2102 GCTTTGGGAGATGATCCCGGGATAGCTTTGTGAGGGGGTTGAGCTTTGCTAGATCTGGG 1381
1324 GGTGATTGGGCGGAGTGTGTTTGTCTTAG 1350
2162 GGTGATTGGGCGGAGTGTGTTTGTCTTAG 2188

RESULT 6
US-10-662-914-11
; Sequence 11, Application US/10662914
; Publication No. US2004012684A1
; GENERAL INFORMATION:
; APPLICANT: Lei, Xingren
; APPLICANT: Mullanev, Edward J
; APPLICANT: Ullah, Abul H.J.
; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTASES
; FILE REFERENCE: 19603/4261
; CURRENT APPLICATION NUMBER: US/10/662,914
; PRIOR FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: 60/410,736
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 2665
; TYPE: DNA
; ORGANISM: Aspergillus niger
US-10-662-914-11

Query Match 99.7%; Score 1345.4; DB 17; Length 2665;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1346; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CTGGCAGTCCCGCCTCGAGAAATCAATCCAGTTCGATACGGTTCGATCAGGGGTATCAA 63
DB 842 CTGGCAGTCCCGCCTCGAGAAATCAATCCAGTTCGATACGGTTCGATCAGGGGTATCAA 901
QY 64 TGCTTCTCGAGACTTCGCATCTTTGGGGTCAATACGACCGCTTCTCTCTGCAAAAC 123
DB 902 TGCTTCTCGAGACTTCGCATCTTTGGGGTCTATACGACCGCTTCTCTCTGCAAAAC 961
QY 124 GAATCGGTATCTCCCTCGAGTCCCGCGATCGAGTCACTTTTCGTCAGTCTCTC 183
DB 962 GAATCGGTATCTCCCTCGAGTCCCGCGATCGAGTCACTTTTCGTCAGTCTCTC 1021
QY 184 TCCCGTCAATGGAGCGGTATCCGACCGACTCCAAAGGCAAGAAATATCTCCGCTCTCAT 243
DB 1022 TCCCGTCAATGGAGCGGTATCCGACCGACTCCAAAGGCAAGAAATATCTCCGCTCTCAT 1081
QY 244 GAGGATCCAGACAGACGCGACCTTTGACGGAATATGCTTCTGAGACATAC 303
DB 1082 GAGGATCCAGACAGACGCGACCTTTGACGGAATATGCTTCTGAGACATAC 1141
QY 304 AACTACAGCTTGGGTGCAGATGACCTGACTCCCTTCGGAGAACAGGAGCTAGTCAACTCC 363
DB 1142 AACTACAGCTTGGGTGCAGATGACCTGACTCCCTTCGGAGAACAGGAGCTAGTCAACTCC 1201
QY 364 GGCATCAAGTTCTACACAGCGGTACGAATCGGTTCACAAAGGAACATCGTTCCATTTCATCCGA 423
DB 1202 GGCATCAAGTTCTACACAGCGGTACGAATCGGTTCACAAAGGAACATCGTTCCATTTCATCCGA 1261
QY 424 TCCTCTGGCTCAGCGCGGTGATCCCTTCGGCAGAAATTCATCGAGGGCTTCAGAGC 483
DB 1262 TCCTCTGGCTCAGCGCGGTGATCCCTTCGGCAGAAATTCATCGAGGGCTTCAGAGC 1321
QY 484 ACCAAGCTGAAGGATCTCTGTCGCCAGCGCGCCCAATCGTCCGCAAGATCGAGTGGTC 543
DB 1322 ACCAAGCTGAAGGATCTCTGTCGCCAGCGCGCCCAATCGTCCGCAAGATCGAGTGGTC 1381
QY 544 ATTTCCGAGGCGAGCTCATCCAAACACATCTCGACCCAGGCACTGCACTGTCTTCGAA 603
DB 1382 ATTTCCGAGGCGAGCTCATCCAAACACATCTCGACCCAGGCACTGCACTGTCTTCGAA 1441
QY 604 GACAGCGAATTCGGCGATACCGTGCAGGCAATTTCCACGCCACGTTGCTCCCTCCATT 663
DB 1442 GACAGCGAATTCGGCGATACCGTGCAGGCAATTTCCACGCCACGTTGCTCCCTCCATT 1501
QY 664 GGTCAACGTCTGGAGACGACCTGTCGGGTGATCTCTCAGACACAGAGTGAACCTAC 723

Db 1502 CGTCAACGCTGGAGAACGACCTGTCCGGTGTGACTCTCACAGACACAGAGTGACCTAC 1561
Qy 724 CTCAATGACATGTCTCTCTTCGACACCATCTCCACGACACCTGTGACACCAAGCTGTCC 783
Db 1562 CTCAATGACATGTCTCTCTTCGACACCATCTCCACGACACCTGTGACACCAAGCTGTCC 1621
Qy 784 CCCCTCTGTGACCTGTTCACCCATGACGATGAGATCACTACGACTACCTCCAGTCTCTTG 843
Db 1622 CCCCTCTGTGACCTGTTCACCCATGACGATGAGATCACTACGACTACCTCCAGTCTCTTG 1681
Qy 844 AAAAAGTATTACGGCCATGTGTGAGTAACCCGCTCGGCCCGGACCCAGGGCGTCCGGCTAC 903
Db 1682 AAAAAGTATTACGGCCATGTGTGAGTAACCCGCTCGGCCCGGACCCAGGGCGTCCGGCTAC 1741
Qy 904 GCTAACGAGCTCATCGCCGCTGTGACCCATCTGCGCTGTCCAGTGTACACAGTTCACAC 963
Db 1742 GCTAACGAGCTCATCGCCGCTGTGACCCATCTGCGCTGTCCAGTGTACACAGTTCACAC 1801
Qy 964 CACACTTTGGACTCGAGCCCGGCTACCTTTCCGCTCAACTCTACTCTCTACGGCGACTTT 1023
Db 1802 CACACTTTGGACTCGAGCCCGGCTACCTTTCCGCTCAACTCTACTCTCTACGGCGACTTT 1861
Qy 1024 TCGCATGACACGGCATCATCTCCATCTCTTTGCTTTAGGCTGTGTACACGGCACTAAG 1083
Db 1862 TCGCATGACACGGCATCATCTCCATCTCTTTGCTTTAGGCTGTGTACACGGCACTAAG 1921
Qy 1084 CCGGTACTACACGACGCTGAGATATACCCAGACAGATGATCTGCTGCTGCTGG 1143
Db 1922 CCGGTACTACACGACGCTGAGATATACCCAGACAGATGATCTGCTGCTGCTGG 1981
Qy 1144 ACGGTTCGCTTGTCTCGCTTGTACGTGAGATGATGACAGTTCAGGGCGGACGAG 1203
Db 1982 ACGGTTCGCTTGTCTCGCTTGTACGTGAGATGATGACAGTTCAGGGCGGACGAG 2041
Qy 1204 CCGGTGCTCGCTGTCTGCTTAAATGATCGGCTTGTCCGCTGATGGTTCGGTTGAT 1263
Db 2042 CCGGTGCTCGCTGTCTGCTTAAATGATCGGCTTGTCCGCTGATGGTTCGGTTGAT 2101
Qy 1264 GCTTTGGGGAGATGTACCCGGGATAGCTTTGTGAGGGGTTGAGCTTTGCTAGATCTGGG 1323
Db 2102 GCTTTGGGGAGATGTACCCGGGATAGCTTTGTGAGGGGTTGAGCTTTGCTAGATCTGGG 2161
Qy 1324 GGTGATTTGGCGGAGTGTCTTTGCTTTAG 1350
Db 2162 GGTGATTTGGCGGAGTGTCTTTGCTTTAG 2188

RESULT 7

US-10-662-914-17
; Sequence 17, Application US/10662914
; Publication No. US20040126844A1
; GENERAL INFORMATION:
; APPLICANT: Lei, Xingen
; APPLICANT: Mullaney, Edward J
; APPLICANT: Ullah, Abul H.J.
; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTASES
; FILE REFERENCE: 19603/4261
; CURRENT APPLICATION NUMBER: US/10/662,914
; PRIOR FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: 60/410,736
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 17
; LENGTH: 2665
; TYPE: DNA
; ORGANISM: Aspergillus niger
US-10-662-914-17

Query Match 99.7%; Score 1345.4; DB 17; Length 2665;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1346; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CTGGGAGTCCCGCCTCGAGAAATCAATCCAGTTGGGATACGGTGCATCAGGGGTATCAA 53
Db 842 CTGGGAGTCCCGCCTCGAGAAATCAATCCAGTTGGGATACGGTGCATCAGGGGTATCAA 901
Qy 64 TGTCTTCTCGAGACTTTCGCTCTTTGGGGTCAATACGACACCGTTCCTCTCTCTGGCAAC 123
Db 902 TGTCTTCTCGAGACTTTCGCTCTTTGGGGTCAATACGACACCGTTCCTCTCTCTGGCAAC 961
Qy 124 GAATCGGTCAATCTCCCTGAGGTGCGCGCGAGATGAGAGTCACTTTGCTGAGGTCTTC 183
Db 962 GAATCGGTCAATCTCCCTGAGGTGCGCGCGAGATGAGAGTCACTTTGCTGAGGTCTTC 1021
Qy 184 TCCCGTCAATGAGCGCGGTATCCGACCGACTCCAAAGGGCAAGAAATATCTCCGCTCTCAT 243
Db 1022 TCCCGTCAATGAGCGCGGTATCCGACCGACTCCGAGGGCAAGAAATATCTCCGCTCTCAT 1081
Qy 244 GAGGAGATCCAGCAGAACCGCAACCTTTGACGAAATATGCTCTTCTGAGAACATAC 303
Db 1082 GAGGAGATCCAGCAGAACCGCAACCTTTGACGAAATATGCTCTTCTGAGAACATAC 1141
Qy 304 AACTACAGCTTTGGGTGAGATGACCTGACTCCCTTCGGAGACAGAGCTAGTCACTCC 363
Db 1142 AACTACAGCTTTGGGTGAGATGACCTGACTCCCTTCGGAGACAGAGCTAGTCACTCC 1201
Qy 364 GGCATCAAGTCTTACCAGCGGTACGAAATCGCTCAACAGGAAATCGTTCCATTCACGA 423
Db 1202 GGCATCAAGTCTTACCAGCGGTACGAAATCGCTCAACAGGAAATCGTTCCATTCACGA 1261
Qy 424 TCCCTCTGGCTCAGACCGCGGTGATCGGCTCCGGCAGAGAAATTCATCGAGGGCTTCAGAGC 483
Db 1262 TCCCTCTGGCTCAGACCGCGGTGATCGGCTCCGGCAGAGAAATTCATCGAGGGCTTCAGAGC 1321
Qy 484 ACCAAGCTCAAGGATCTCTGTCGCCAGCCGCGCAATCGTCCGCCAAGATCGACGTGGTC 543
Db 1322 ACCAAGCTCAAGGATCTCTGTCGCCAGCCGCGCAATCGTCCGCCAAGATCGACGTGGTC 1381
Qy 544 ATTTCCAGGGCGAGTCTATCCAAACACTCTCGACCCAGGCACTGCACTGTCTTCGAA 603
Db 1382 ATTTCCAGGGCGAGTCTATCCAAACACTCTCGACCCAGGCACTGCACTGTCTTCGAA 1441
Qy 604 GACNGGAAATTCGGCGATACCGTTCGAAGCAATTTTCACGCCACGTTGTCCTCCCTCCATT 663
Db 1442 GACNGGAAATTCGGCGATACCGTTCGAAGCAATTTTCACGCCACGTTGTCCTCCCTCCATT 1501
Qy 664 CGTCAACGCTCTGGAGAACGACCTGTCCGGTGTGACTCTCACAGACACAGAGTGCCTAC 723
Db 1502 CGTCAACGCTCTGGAGAACGACCTGTCCGGTGTGACTCTCACAGACACAGAGTGCCTAC 1561
Qy 724 CTCATGGACATGTCTCTCTTCACACCATCTCCACAGCACCGTGCACACCGAGTGTCC 783
Db 1562 CTCATGGACATGTCTCTCTTCACACCATCTCCACAGCACCGTGCACACCGAGTGTCC 1621
Qy 784 CCCTTCTGTGACTGTTCACCCATGCAAGATGGATCACTACGACTACCTCCAGTCTCTTG 843
Db 1622 CCCTTCTGTGACTGTTCACCCATGCAAGATGGATCACTACGACTACCTCCAGTCTCTTG 1681
Qy 844 AAAAGTATTACGGCGATGTCAGGTAAACCGCTCGGCCCGGACCCAGGGCGTCCGGCTAC 903
Db 1682 AAAAGTATTACGGCGATGTCAGGTAAACCGCTCGGCCCGGACCCAGGGCGTCCGGCTAC 1741
Qy 904 GCTAACGAGCTCATCGCCGCTGTGACCCACTCGCTGTCCAGATGACACAGTTCACAC 963
Db 1742 GCTAACGAGCTCATCGCCGCTGTGACCCACTCGCTGTCCAGATGACACAGTTCACAC 1801
Qy 964 CACACTTTGGACTCGAGCCCGGCTACCTTTCCGCTCAACTCTACTCTCTACCGGACTTT 1023
Db 1802 CACACTTTGGACTCGAGCCCGGCTACCTTTCCGCTCAACTCTACTCTCTACCGGACTTT 1861
Qy 1024 TCGCATGACACGGCATCATCTCTTTGCTTTAGGCTGTGTACAAAGGCACTAAG 1083
Db 1862 TCGCATGACACGGCATCATCTCTTTGCTTTAGGCTGTGTACAAAGGCACTAAG 1921
Qy 1084 CCGCTATCTACCCAGCGGTGAGTATACCCAGACAGATGATCTGCTGCTGCTGG 1143

Db 1922 CGGCTATCTACACAGCGTGGAGAAATACCCAGACAGATGATCTCGTCTGCTGG 1981
Qy 1144 AGGTTCCGTTTGGTTCGGTTTGTACGTCAGATGATGAGTCTCAGGCGGAGCAGAG 1203
Db 1982 AGGTTCCGTTTGGTTCGGTTTGTACGTCAGATGATGAGTCTCAGGCGGAGCAGAG 2041
Qy 1204 CGGCTGGTCCGTTTGGTTCGTTTAAATGATCGCTTGTCCCGCTGCAATGGTGTCCGTTTGTAT 1263
Db 2042 CGGCTGGTCCGTTTGGTTCGTTTAAATGATCGCTTGTCCCGCTGCAATGGTGTCCGTTTGTAT 2101
Qy 1264 GCTTTGGGAGATGATPACCCGGGATAGCTTTGTGAGGGGTTGAGCTTTGTAGATCTGGG 1323
Db 2102 GCTTTGGGAGATGATPACCCGGGATAGCTTTGTGAGGGGTTGAGCTTTGTAGATCTGGG 2161
Qy 1324 GGTGATTGGCGGAGTGTCTTGGCTTAG 1350
Db 2162 GGTGATTGGCGGAGTGTCTTGGCTTAG 2188

RESULT 8

US-10-662-914-19
; Sequence 19, Application US/10662914
; Publication No. US2004012684A1
; GENERAL INFORMATION:
; APPLICANT: Lei, Xingen
; APPLICANT: Mullaney, Edward J
; APPLICANT: Ullah, Abul H.J.
; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTASES
; FILE REFERENCE: 19603/4261
; CURRENT APPLICATION NUMBER: US/10/662,914
; CURRENT FILING DATE: 2003-09-15
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 2665
; TYPE: DNA
; ORGANISM: Aspergillus niger
US-10-662-914-19

Query Match 99.7%; Score 1345.4; DB 17; Length 2665;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1346; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CTGGCAGTCCCGGCTCGAGAAATCAATCCAGTTGCGATACGTCGATCAGGGGTATCAA 63
Db 842 CTGGCAGTCCCGGCTCGAGAAATCAATCCAGTTGCGATACGTCGATCAGGGGTATCAA 901
Qy 64 TGCTTCCGAGACTTCGATCTTTGGGGTCAATACGACCGCTTCTCTCTCTGGCAAC 123
Db 902 TGCTTCCGAGACTTCGATCTTTGGGGTCAATACGACCGCTTCTCTCTCTGGCAAC 961
Qy 124 GAATCGGTATCTCCCTGAGGTGCCCGCGGATCGAGATCACTTTGCTCAGGTCCCTC 183
Db 962 GAATCGGTATCTCCCTGAGGTGCCCGCGGATCGAGATCACTTTGCTCAGGTCCCTC 1021
Qy 184 TCCGTCATGAGCGCGGTATCCGACCGACTCCAAAGGCAAGAAATCTCCGCTCTCAT 243
Db 1022 TCCGTCATGAGCGCGGTATCCGACCGACTCCAAAGGCAAGAAATCTCCGCTCTCAT 1081
Qy 244 GAGGAGATCCAGAGACCGCAACCTTTTGAACGAAATATGCTTCTCTGAAGACATAC 303
Db 1082 GAGGAGATCCAGAGACCGCAACCTTTTGAACGAAATATGCTTCTCTGAAGACATAC 1141
Qy 304 AACTACAGTTTGGTGCAGATGACTGACTCCCTTCGAGAACAGAGCTAGTCACTCC 363
Db 1142 AACTACAGTTTGGTGCAGATGACTGACTCCCTTCGAGAACAGAGCTAGTCACTCC 1201
Qy 364 GGCATCAAGTTCTACACGCGGTAGCAATCGCTCAAGAGAACATCGTTTCCATTCAATCCGA 423
Db 1202 GGCATCAAGTTCTACACGCGGTAGCAATCGCTCAAGAGAACATCGTTTCCATTCAATCCGA 1261

RESULT 9

US-10-662-914-21
; Sequence 21, Application US/10662914
; Publication No. US2004012684A1
; GENERAL INFORMATION:
; APPLICANT: Lei, Xingen
; APPLICANT: Mullaney, Edward J

APPLICANT:	Ullah, Abul H. J.
TITLE OF INVENTION:	USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTASES
FILE REFERENCE:	19603/4261
CURRENT APPLICATION NUMBER:	US/10/662,914
CURRENT FILING DATE:	2003-09-15
PRIOR APPLICATION NUMBER:	60/410,736
PRIOR FILING DATE:	2002-09-13
NUMBER OF SEQ ID NOS:	69
SOFTWARE:	Patentin Ver. 2.1
SEQ ID NO 21	
LENGTH:	2665
TYPE:	DNA
ORGANISM:	Aspergillus niger
US-10-662-914-21	
Query Match	99.7%; Score 1345.4; DB 17; Length 2665;
Best Local Similarity	95.9%; Pred. No. 0;
Matches 1346; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
QY	4 CTGSCAGTCCCGCCTCGAGAAATCAATCCAGTTGCGATACGGTTCGATCAGGGGTATCAA 63
Db	842 CTGSCAGTCCCGCCTCGAGAAATCAATCCAGTTGCGATACGGTTCGATCAGGGGTATCAA 901
QY	64 TGTCTTCCGAGACTTCGCATCTTTGGGGTCAATACGACCGGTTCTTCTCTCGCAAC 123
Db	902 TGTCTTCCGAGACTTCGCATCTTTGGGGTCAATACGACCGGTTCTTCTCTCGCAAC 961
QY	124 GATTCGGTTCATCTCCCTCGAGTGCCTCCGCGGATGCGAGTCACTTTCGTCAGTCTC 183
Db	962 GATTCGGTTCATCTCCCTCGAGTGCCTCCGCGGATGCGAGTCACTTTCGTCAGTCTC 1021
QY	184 TCCCGTTCATGGAGCGCGGTATCCGACCGACTCCAAAGCGCAAGAAATACTTCGGTCTCAT 243
Db	1022 TCCCGTTCATGGAGCGCGGTATCCGACCGACTCCAAAGCGCAAGAAATACTTCGGTCTCAT 1081
QY	244 GAGGAGATCCAGAGAACGGACACACCTTTGAACGAAATATGCTCTCTGAAGACATAC 303
Db	1082 GAGGAGATCCAGAGAACGGACACACCTTTGAACGAAATATGCTCTCTGAAGACATAC 1141
QY	304 AACTACAGCTTGGGTGCAGATGACTGCATCCCTTCGGAGAACAGGAGCTAGTCAACTCC 363
Db	1142 AACTACAGCTTGGGTGCAGATGACTGCATCCCTTCGGAGAACAGGAGCTAGTCAACTCC 1201
QY	364 GGCATCAAGTTTACACGCGGTACGAATCGTCTCAAGAGAACATCGTTTCATTCATCCGA 423
Db	1202 GGCATCAAGTTTACACGCGGTACGAATCGTCTCAAGAGAACATCGTTTCATTCATCCGA 1261
QY	424 TCCTCTGGCTCCAGCCGCGTATCGCTCCGGCAAGAAATTCATCGAGGGCTCCAGAC 483
Db	1262 TCCTCTGGCTCCAGCCGCGTATCGCTCCGGCAAGAAATTCATCGAGGGCTCCAGAC 1321
QY	484 ACCAAGTGAAGGATCTCTGTGCCAGCCGGCCAAATCGTCGCCCAAGATCGAGTGGTC 543
Db	1322 ACCAAGTGAAGGATCTCTGTGCCAGCCGGCCAAATCGTCGCCCAAGATCGAGTGGTC 1381
QY	544 ATTTCGAGCGCAGCTCATCCAAACACATCTCGACCCAGGACCTGCATGTCTTCGAA 603
Db	1382 ATTTCGAGCGCAGCTCATCCAAACACATCTCGACCCAGGACCTGCATGTCTTCGAA 1441
QY	604 GACAGCGAAATTGGCCGATACCGTTCGAAGCCAAATTCACCGCCAGTTCGTCCTCCCTCCATT 663
Db	1442 GACAGCGAATTGGCCGATACCGTTCGAAGCCAAATTCACCGCCAGTTCGTCCTCCCTCCATT 1501
QY	664 CGTCAACGCTTGAGAGACGACCTGTCCGGTGTGACTCTCAAGACAGAAAGTGACCTAC 723
Db	1502 CGTCAACGCTTGAGAGACGACCTGTCCGGTGTGACTCTCAAGACAGAAAGTGACCTAC 1561
QY	724 CTCATGACATGTGCTCTCTTCGACACCATCTCCACAGACCGGTCGACACCAAGCTGTCC 783
Db	1562 CTCATGACATGTGCTCTCTTCGACACCATCTCCACAGACCGGTCGACACCAAGCTGTCC 1621
QY	784 CCCTTCGTGACCTGTTTCA CCCATGACGAATGGATCAACTACGACTACCTCCAGTCTTG 843

Db	1622	CCCTTCGTGTGACCTGTTTCA	CCCAATGACGAATGGATCAACTACGACTACCTCCAGTCCCTTG	1681
Qy	844	AAAAAGATTATTACGGCCATGGTGCAGGTAA	CCCGCTCGCGCCCGAGCCCAACAGGCGCTCGGCTAC	903
Db	1682	AAAAAGATTATTACGGCCATGGTGCAGGTAA	CCCGCTCGCGCCCGAGCCCAACAGGCGCTCGGCTAC	1741
Qy	904	GCTAACGAGCTCATCGCGCGCTGTGACCA	CTCGCCTGTCCACGATGACACAGTTCCAAC	963
Db	1742	GCTAACGAGCTCATCGCGCGCTGTGACCA	CTCGCCTGTTCACGATGACACAGTTCCAAC	1801
Qy	964	CACACTTTGGACTCGAGCCCGGCTACCTTT	CCGCTCAAACTCTACTCTCTACGCGGACTTTT	1023
Db	1802	CACACTTTGGACTCGAGCCCGGCTACCTTT	CCGCTCAAACTCTACTCTCTACGCGGACTTTT	1861
Qy	1024	TCGCATGACAACGGCATCATCTCCATCTCT	TTTGTCTTTAGGCTGTGACACGGCACTAAG	1083
Db	1862	TCGCATGACAACGGCATCATCTCCATCTCT	TTTGTCTTTAGGCTGTGACACGGCACTAAG	1921
Qy	1084	CCGCTATCTACCAACGACCGTGGAGATAT	CACCCAGACAGATGGATTTCTCGTCTGTGG	1143
Db	1922	CCGCTATCTACCAACGACCGTGGAGATAT	CACCCAGACAGATGGATTTCTCGTCTGTGG	1981
Qy	1144	ACGGTTCCGTTTGGTTCGCTTTGTAGCTCG	AGATGACAGTGTCAAGCGGAGCAGGAG	1203
Db	1982	ACGGTTCCGTTTGGTTCGCTTTGTAGCTCG	AGATGACAGTGTCAAGCGGAGCAGGAG	2041
Qy	1204	CCGCTGCTCGGTGTCTTTGGTTAATGATCG	CGGTTGTCCCGTGCATGGGTTCGCGTTGAT	1263
Db	2042	CCGCTGCTCGGTGTCTTTGGTTAATGATCG	CGGTTGTCCCGTGCATGGGTTCGCGTTGAT	2101
Qy	1264	GCITTTGGGAGATGTACCCGGATAGCTTT	GTGTGAGGGGTTGAGCTTGTCTAGATCTGG	1323
Db	2102	GCITTTGGGAGATGTACCCGGATAGCTTT	GTGTGAGGGGTTGAGCTTGTCTAGATCTGG	2161
Qy	1324	GGTGATTGGCGGAGTGTCTTTTGCTTAG	1350	
Db	2162	GGTGATTGGCGGAGTGTCTTTTGCTTAG	2188	
RESULT 10				
US-10-662-914-23				
; Sequence 23, Application US/10662914				
; Publication No. US20040126844A1				
; GENERAL INFORMATION:				
; APPLICANT: Lei, Xingwen				
; APPLICANT: Mallaney, Edward J				
; APPLICANT: Ullah, Abul H.J.				
; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTASES				
; FILE REFERENCE: 19603/4261				
; CURRENT APPLICATION NUMBER: US/10/662,914				
; CURRENT FILING DATE: 2003-09-15				
; PRIOR APPLICATION NUMBER: 60/410,736				
; PRIOR FILING DATE: 2002-09-13				
; NUMBER OF SEQ ID NOS: 69				
; SOFTWARE: Fatentin ver. 2.1				
; SEQ ID NO 23				
; LENGTH: 2665				
; TYPE: DNA				
; ORGANISM: Aspergillus niger				
US-10-662-914-23				

	Query Match	99.7%;	Score 1345.4;	DB 17;	Length 2665;
	Best Local Similarity	99.9%;	Pred. No. 0;		
	Matches 1346;	Conservative	0;	Mismatches	1;
				Indels	0;
				Gaps	0;
Qy	4	CTGGCAGTCCCGCCCTCGAGAAATCAATCAGTTGCGATACGGT	CGATCGATCAGGGGTATCAA	63	
Db	842	CTGGCAGTCCCGCCCTCGAGAAATCAATCAGTTGCGATACGGT	CGATCAGGGGTATCAA	901	
Qy	64	TGCTTCTCGGAGACTTCGCACTTTTGGGGTCAATACGACCGGTT	CTTCTCTCTGGCAAAAC	123	
Db	902	TGCTTCTCGGAGACTTCGCACTTTTGGGGTCAATACGACCGGTT	CTTCTCTCTGGCAAAAC	961	

124 GAATCGGTGATCTCCCTGAGTCCCGCGGATGACAGATGCACTTTCGCTCAGGTCCTC 183
Db
962 GAATCGGTGATCTCCCTGAGTCCCGCGGATGACAGATGCACTTTCGCTCAGGTCCTC 1021
QY
184 TCCGCTCATGAGCGCGGTATCCGACGATCTCAAGGGCAAGAAATGCTTCGCTCCTCAT 243
Db
1022 TCCGCTCATGAGCGCGGTATCCGACGATCTCAAGGGCAAGAAATGCTTCGCTCCTCAT 1081
QY
244 GAGGAGATCCAGCAGACGCGACCACTTTGACGGAATAATGCTTCCTGGAAGACATAC 303
Db
1082 GAGGAGATCCAGCAGACGCGACCACTTTGACGGAATAATGCTTCCTGGAAGACATAC 1141
QY
304 AACTACAGCTTGGGTGACAGATGACCTGATCCTCTTCGAGAAACAGGAGCTAGTCACTCC 363
Db
1142 AACTACAGCTTGGGTGACAGATGACCTGATCCTCTTCGAGAAACAGGAGCTAGTCACTCC 1201
QY
364 GGCATCAAGTTCTACCGGCTGACGAATCGCTCAAGAGAACATCGTTCCATTCATCCGA 423
Db
1202 GGCATCAAGTTCTACCGGCTGACGAATCGCTCAAGAGAACATCGTTCCATTCATCCGA 1261
QY
424 TCCTCTGGCTCCAGCGCGTGAATCGCTCCGCAAGAAATTCATCGAGGCTTCCAGAGC 483
Db
1262 TCCTCTGGCTCCAGCGCGTGAATCGCTCCGCAAGAAATTCATCGAGGCTTCCAGAGC 1321
QY
484 ACCAAGCTGAAGGATCTCGTCCGAGCGCGGCAATCGTCGCGCAAGATCGAGCTGGTC 543
Db
1322 ACCAAGCTGAAGGATCTCGTCCGAGCGCGGCAATCGTCGCGCAAGATCGAGCTGGTC 1381
QY
544 ATTTCCGAGGCGAGCTCATCAACAACTCTCGACCCAGGCACTGCACTGCTTCGAA 603
Db
1382 ATTTCCGAGGCGAGCTCATCAACAACTCTCGACCCAGGCACTGCACTGCTTCGAA 1441
QY
604 GACAGCGAATTTGGCGATACCGTCCGAGGCAATTTACCGCGCAGGTCGTCCTCCATTC 663
Db
1442 GACAGCGAATTTGGCGATACCGTCCGAGGCAATTTACCGCGCAGGTCGTCCTCCATTC 1501
QY
664 CGTCAAGCTCTGGAGACGACCTGTCGCGTGTGACTCTCAGACACAGAAAGTACCTAC 723
Db
1502 CGTCAAGCTCTGGAGACGACCTGTCGCGTGTGACTCTCAGACACAGAAAGTACCTAC 1561
QY
724 CTCATGGAATGTGCTCTCGACACCAATCTCCACGACCGTTCGACACCAAGCTGTCC 783
Db
1562 CTCATGGAATGTGCTCTCGACACCAATCTCCACGACCGTTCGACACCAAGCTGTCC 1621
QY
784 CCTTCTGTGACCTGTCACCCATGACGAATGGAATCACTACGATCACTCCAGTCTCTG 843
Db
1622 CCTTCTGTGACCTGTCACCCATGACGAATGGAATCACTACGATCACTCCAGTCTCTG 1681
QY
844 AAAAGTATTACGGCCATGTTGACAGGTAAACCGCTCCGCGCCGACCCAGGCGGTGCGTAC 903
Db
1682 AAAAGTATTACGGCCATGTTGACAGGTAAACCGCTCCGCGCCGACCCAGGCGGTGCGTAC 1741
QY
904 GCTAACGAGCTCATGCGCGCTGACCCACTGCGCTGTCCAGATGACACAGGTTCCAAAC 963
Db
1742 GCTAACGAGCTCATGCGCGCTGACCCACTGCGCTGTCCAGATGACACAGGTTCCAAAC 1801
QY
964 CACACTTTGGACTCGAGCGCGCTACCTTTCCGCTCAACTCTACTCTCTACGCGGACTTT 1023
Db
1802 CACACTTTGGACTCGAGCGCGCTACCTTTCCGCTCAACTCTACTCTCTACGCGGACTTT 1861
QY
1024 TCGAATGACACGCGATCATCTCCATTCCTTTGCTTTAGTCTGTGACACGCGACTAAG 1083
Db
1862 TCGAATGACACGCGATCATCTCCATTCCTTTGCTTTAGTCTGTGACACGCGACTAAG 1921
QY
1084 CGGCTATCTACACGACCGTGGAGAAATCAACCCAGACAGATGATGATCTCGTCTGCTTG 1143
Db
1922 CGGCTATCTACACGACCGTGGAGAAATCAACCCAGACAGATGATGATCTCGTCTGCTTG 1981
QY
1144 ACGGTTCCGTTTGTCTCGCTTTGTACGTCAGATGATGACAGTGTACAGGCGGACGAG 1203
Db
1982 ACGGTTCCGTTTGTCTCGCTTTGTACGTCAGATGATGACAGTGTACAGGCGGACGAG 2041
QY
1204 CGGCTGTCGCTGTCTTGGTTAAATGATCGCTGTGTCGCGTGTGTCGCGCTGATGCGTTC 1263

2042 CCGCTGGTCCGCTGCTTGGTTAAATGATCGCTTCCGCTGCAATGGGTGCCGGTTGAT 2101
QY
1264 GCTTTGGGAGATGATACCCGGATAGCTTTGCTGAGGGGTTGAGCTTTGCTAGATCTGGG 1323
Db
2102 GCTTTGGGAGATGATACCCGGATAGCTTTGCTGAGGGGTTGAGCTTTGCTAGATCTGGG 2161
QY
1324 GGTGATTCGGCGGAGTGTTCCTTAG 1350
Db
2162 GGTGATTCGGCGGAGTGTTCCTTAG 2188
RESULT 11
US-10-662-914-25
; Sequence 25, Application US/10662914
; Publication No. US2004012684A1
; GENERAL INFORMATION:
; APPLICANT: Lei, Xingen
; APPLICANT: Mullaney, Edward J
; APPLICANT: Ullah, Abul H.J.
; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTASES
; FILE REFERENCE: 19603/4261
; CURRENT APPLICATION NUMBER: US/10/662,914
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: 60/410,736
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 2665
; TYPE: DNA
; ORGANISM: Aspergillus niger
US-10-662-914-25
Query Match 99.7%; Score 1345.4; DB 17; Length 2665;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1346; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4 CTGGCAGTCCCGCTCGAGAAATCAATCCAGTTTCGATAGCGTTCGATCAGGGGTATCAA 63
Db 842 CTGGCAGTCCCGCTCGAGAAATCAATCCAGTTTCGATAGCGTTCGATCAGGGGTATCAA 901
QY 64 TCGTCTCGAGACTTCGCACTTTGGGGTCAATACGACCGTTCCTCTCTGCGCAAC 123
Db 902 TCGTCTCGAGACTTCGCACTTTGGGGTCAATACGACCGTTCCTCTCTGCGCAAC 961
QY 124 GAATCGTCACTCCCTCGAGTCCCGCGGATCGAGTCACTTTTCGCTCAGTCTCTC 183
Db 962 GAATCGTCACTCCCTCGAGTCCCGCGGATCGAGTCACTTTTCGCTCAGTCTCTC 1021
QY 184 TCCGCTCATGAGCGGCTATCCGACCGATCCAAAGGCAAGAAATATCTCGCTCTCAT 243
Db 1022 TCCGCTCATGAGCGGCTATCCGACCGATCCAAAGGCAAGAAATATCTCGCTCTCAT 1081
QY 244 GAGGAGATCCAGCAGACGCGACCTTTGACGGAATAATGCTTCCTGGAAGACATAC 303
Db 1082 GAGGAGATCCAGCAGACGCGACCTTTGACGGAATAATGCTTCCTGGAAGACATAC 1141
QY 304 AACTACAGCTTGGGTGACAGATGACCTGATCCTCTTCGAGAAACAGGAGCTAGTCACTCC 363
Db 1142 AACTACAGCTTGGGTGACAGATGACCTGATCCTCTTCGAGAAACAGGAGCTAGTCACTCC 1201
QY 364 GGCATCAAGTTCTACCGGCTGACGAATCGCTCAAGAGAACATCGTTCCATTCATCCGA 423
Db 1202 GGCATCAAGTTCTACCGGCTGACGAATCGCTCAAGAGAACATCGTTCCATTCATCCGA 1261
QY 424 TCCTCTGGCTCCAGCGCGTGAATCGCTCCGCAAGAAATTCATCGAGGCTTCCAGAGC 483
Db 1262 TCCTCTGGCTCCAGCGCGTGAATCGCTCCGCAAGAAATTCATCGAGGCTTCCAGAGC 1321
QY 484 ACCAAGCTGAAGGATCTCGTCCGAGCGCGGCAATCGTCCGCAAGATCGAGCTGGTC 543
Db 1322 ACCAAGCTGAAGGATCTCGTCCGAGCGCGGCAATCGTCCGCAAGATCGAGCTGGTC 1381

Qy	544	ATTTCCGAGGCGAGCTCATCCAAACACACTCTCGACCCAGGCACTCGACTGCTTCGAA	603
Db	1382	ATTTCCGAGGCGAGCTCATCCAAACACACTCTCGACCCAGGCACTCGACTGCTTCGAA	1441
Qy	604	GACAGCGAATTGGCCGATACCGTCCGAAGCCAAATTTACCGGCCAGTTTCGTCCCTCCATT	663
Db	1442	GACAGCGAATTGGCCGATACCGTCCGAAGCCAAATTTACCGGCCAGTTTCGTCCCTCCATT	1501
Qy	664	CGTCAAAGCTCTGGAGAGGACCTGTCGGGTGTGACTCTCAGACACAGAAAGTGACCTAC	723
Db	1502	CGTCAAAGCTCTGGAGAGGACCTGTCGGGTGTGACTCTCAGACACAGAAAGTGACCTAC	1561
Qy	724	CTCATGACATGTGCTCTCTTCGACACCATCTTCACACAGACCGGTCCGACACCAAGCTGCC	783
Db	1562	CTCATGACATGTGCTCTCTTCGACACCATCTTCACACAGACCGGTCCGACACCAAGCTGCC	1621
Qy	784	CCCTTCTGACCTGTTACCGATGACGATGAGATCAACTAGACTACCTCCAGTCCCTTG	843
Db	1622	CCCTTCTGACCTGTTACCGATGACGATGAGATCAACTAGACTACCTCCAGTCCCTTG	1681
Qy	844	AAAAAGATTATACGGCCATGTGACAGGTAAACCGGTCCGCCCGACCCAGGCGCTCGGCTAC	903
Db	1682	AAAAAGATTATACGGCCATGTGACAGGTAAACCGGTCCGCCCGACCCAGGCGCTCGGCTAC	1741
Qy	904	GCTTAAAGAGTCTATGCGCCGCTGTGACCCATCGCCCTGTCCACGATGACACGAGTCCAAC	963
Db	1742	GCTTAAAGAGTCTATGCGCCGCTGTGACCCATCGCCCTGTCCACGATGACACGAGTCCAAC	1801
Qy	964	CACACTTTGACTCGAGCCCGGCTACCTTTCCGCTCAACTCTACTCTCTACGCGGACTTTT	1023
Db	1802	CACACTTTGACTCGAGCCCGGCTACCTTTCCGCTCAACTCTACTCTCTACGCGGACTTTT	1861
Qy	1024	TGCGATGACAAACGGCATCATCTCCATCTCTTTTGGCTTGTATACAGGCACTAAG	1083
Db	1862	TGCGATGACAAACGGCATCATCTCCATCTCTTTTGGCTTGTATACAGGCACTAAG	1921
Qy	1084	CCGCTATCTACACGACCGGTGGAGATATACCCAGACAGATGGATTTCTGCTGCTTGG	1143
Db	1922	CCGCTATCTACACGACCGGTGGAGATATACCCAGACAGATGGATTTCTGCTGCTTGG	1981
Qy	1144	ACGGTTCCGGTTTGGCTTTCGGCTTTGTACGTGAGATGATGACAGTGTGAGGCGGACGAG	1203
Db	1982	ACGGTTCCGGTTTGGCTTTCGGCTTTGTACGTGAGATGATGACAGTGTGAGGCGGACGAG	2041
Qy	1204	CCGCTGGTCCGTGCTTGGTTTAAATGATCGGGTTGTCCCGTGCATGGGTGTCGGTTGAT	1263
Db	2042	CCGCTGGTCCGTGCTTGGTTTAAATGATCGGGTTGTCCCGTGCATGGGTGTCGGTTGAT	2101
Qy	1264	GCCTTTGGGAGATGTATCCCGGATAGCTTTTTCAGGGGGTTGAGCTTTGCTAGATCTGG	1323
Db	2102	GCCTTTGGGAGATGTATCCCGGATAGCTTTTTCAGGGGGTTGAGCTTTGCTAGATCTGG	2161
Qy	1324	GCTGATTTGGCGGAGTGTTTTGGCTTAG	1350
Db	2162	GCTGATTTGGCGGAGTGTTTTGGCTTAG	2188

RESULT 12
US-10-662-914-27
/ Sequence 27, Application US/10662914
/ Publication No. US20040126844A1
/ GENERAL INFORMATION:
/ APPLICANT: Lei, Xingen
/ APPLICANT: Mullaney, Edward J
/ APPLICANT: Ullah, Abul H.J.
/ TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTASES
/ FILE REFERENCE: 19603/4261
/ CURRENT APPLICATION NUMBER: US/10/662,914
/ CURRENT FILING DATE: 2003-09-15
/ PRIOR APPLICATION NUMBER: 60/410,736
/ PRIOR FILING DATE: 2002-09-13
/ NUMBER OF SEQ ID NOS: 69

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 2665
; TYPE: DNA
; ORGANISM: Aspergillus niger
US-10-662-914-27

```

Query Match 99.7%; Score 1345.4; DB 17; Length 2665;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1345; Conservative 0; Mismatches 1; Indels 0;

QY	4	CTGGCAGTCCCGCGCTCGAGAAATCAATCAGTTGGATACGGTCGATACGGGGTATCAA	63
Db	842	CTGGCAGTCCCGCGCTCGAGAAATCAATCAGTTGGATACGGTCGATACGGGGTATCAA	901
QY	64	TGCTTCTCCGAGACTTCGCATCTTTGGGTCAATACGCACGGTTCTTCTCTCTGGCAAA	123
Db	902	TGCTTCTCCGAGACTTCGCATCTTTGGGTCAATACGCACGGTTCTTCTCTCTGGCAAA	961
QY	124	GAATCGGTCACTCTCCCTGAGGTGCCCGCGGATGCAAGTCACTTTTCGTCTAGGTCTCT	183
Db	962	GAATCGGTCACTCTCCCTGAGGTGCCCGCGGATGCAAGTCACTTTTCGTCTAGGTCTCT	1021
QY	184	TCCCGTCATCGAGCGCGGTATCCGACCGACTTCCAAGGGCAAGAAATACTCCGCTCTCAT	243
Db	1022	TCCCGTCATCGAGCGCGGTATCCGACCGACTTCCAAGGGCAAGAAATACTCCGCTCTCAT	1081
QY	244	GAGGAGATCAGCAGAAACGGCAACAACCTTTGACGGAATAATGCTTCTCTGAAGACATAC	303
Db	1082	GAGGAGATCAGCAGAAACGGCAACAACCTTTGACGGAATAATGCTTCTCTGAAGACATAC	1141
QY	304	AACTACAGCTTGGGTGCAGATGACTGACTCCCTTCGGAGAACGAGAGCTAGTCAACTCC	363
Db	1142	AACTACAGCTTGGGTGCAGATGACTGACTCCCTTCGGAGAACGAGAGCTAGTCAACTCC	1201
QY	364	GGCATCAAGTTCTACAGCGGTACGAATCGCTCACAAAGGAACAATCGTTCCATTTCATCCGA	423
Db	1202	GGCATCAAGTTCTACAGCGGTACGAATCGCTCACAAAGGAACAATCGTTCCATTTCATCCGA	1261
QY	424	TCCTCTGGCTCCAGCGCGGTATCGCTCCCGCAAGAAATTCATCAGAGGCTTCCAGAGC	483
Db	1262	TCCTCTGGCTCCAGCGCGGTATCGCTCCCGCAAGAAATTCATCAGAGGCTTCCAGAGC	1321
QY	484	ACCAAGCTGAAGATCTCTGTGCCACAGCGCGCAATCGTTCGCCCAAGATCGACGTGGTC	543
Db	1322	ACCAAGCTGAAGATCTCTGTGCCACAGCGCGCAATCGTTCGCCCAAGATCGACGTGGTC	1381
QY	544	ATTTCGAGGCCAGCTCATCCAAACAACCTCTCGACCCAGGACCTGCACTGTCTTCGAA	603
Db	1382	ATTTCGAGGCCAGCTCATCCAAACAACCTCTCGACCCAGGACCTGCACTGTCTTCGAA	1441
QY	604	GACAGCGAATTGGCCGATACCGTCGAAGCAATTTCAACCGCAAGTTTCGTCCCTCCATT	663
Db	1442	GACAGCGAATTGGCCGATACCGTCGAAGCAATTTCAACCGCAAGTTTCGTCCCTCCATT	1501
QY	664	CGTCAACGCTCGGAGAACACCTGTCCGTTGTGACTCTCACAGACACAGAAGTGACCTAC	723
Db	1502	CGTCAACGCTCGGAGAACACCTGTCCGTTGTGACTCTCACAGACACAGAAGTGACCTAC	1561
QY	724	CTCATGGAATGTGCTCTTGGACACATCTCCACAGCACCGTTCGACCAAGCTGTCTC	783
Db	1562	CTCATGGAATGTGCTCTTGGACACATCTCCACAGCACCGTTCGACCAAGCTGTCTC	1621
QY	784	CCCTTCTGTGACTGTTCACCATGACGAATGATCAACTACGACTACCTCCAGTCTCTTG	843
Db	1622	CCCTTCTGTGACTGTTCACCATGACGAATGATCAACTACGACTACCTCCAGTCTCTTG	1681
QY	844	AAAAAGTATTACGGCCATGGTGCAGTAACCGCTCGGCCCGACCCAGGGGCTCGCTAC	903
Db	1682	AGAAAGTATTACGGCCATGGTGCAGTAACCGCTCGGCCCGACCCAGGGGCTCGCTAC	1741
QY	904	GCTAACGAGCTCATCCCGCTCTGACCCACTCGCTGTCCAGATGACACCAAGTTCACAC	963

Db 1742 GCTAAAGAGCTCATCGCCGCTGACGCCACTCGCTCTCCACGATGACACCAAGTTCCAAAC 1801
Qy 964 CACACTTTGGACTCGAGCCGGCTACCTTTCCGCTCAACTCTACTCTCTACGGGACTTT 1023
Db 1802 CACACTTTGGACTCGAGCCGGCTACCTTTCCGCTCAACTCTACTCTCTACGGGACTTT 1861
Qy 1024 TCGCATGACAAACGGCATCATCTCCATTCTCTTTTGGTTTGGTTTGGTTTGGTTTGGTTT 1083
Db 1862 TCGCATGACAAACGGCATCATCTCCATTCTCTTTTGGTTTGGTTTGGTTTGGTTTGGTTT 1921
Qy 1084 CCGTATCTACACGACGGTGGAGAAATCACCCAGACAGATGATCTCGTCTGCTTGG 1143
Db 1922 CCGTATCTACACGACGGTGGAGAAATCACCCAGACAGATGATCTCGTCTGCTTGG 1981
Qy 1144 ACGGTTCCGTTTGGTTTGGTTTGGTTTGGTTTGGTTTGGTTTGGTTTGGTTTGGTTTGG 1203
Db 1982 ACGGTTCCGTTTGGTTTGGTTTGGTTTGGTTTGGTTTGGTTTGGTTTGGTTTGGTTTGG 2041
Qy 1204 CCGTGGTCCGTTTGGTTTGGTTTGGTTTGGTTTGGTTTGGTTTGGTTTGGTTTGGTTTGG 1263
Db 2042 CCGTGGTCCGTTTGGTTTGGTTTGGTTTGGTTTGGTTTGGTTTGGTTTGGTTTGGTTTGG 2101
Qy 1264 GCTTTGGGAGATGATACCCGGGATAGCTTTGTGAGGGGTTGAGCTTTGTAGATCTGGG 1323
Db 2102 GCTTTGGGAGATGATACCCGGGATAGCTTTGTGAGGGGTTGAGCTTTGTAGATCTGGG 2161
Qy 1324 GGTGATTGGCGGAGTGTGTTGCTTAG 1350
Db 2162 GGTGATTGGCGGAGTGTGTTGCTTAG 2188

RESULT 13

US-10-662-914-29
; Sequence 29, Application US/10662914
; Publication No. US20040126844A1
; GENERAL INFORMATION:
; APPLICANT: Mullaney, Edward J
; APPLICANT: Ullah, Abdul H.J.
; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTASES
; FILE REFERENCE: 19603/4261
; CURRENT APPLICATION NUMBER: US/10/662,914
; PRIORITY FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: 60/410,736
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 29
; LENGTH: 2665
; TYPE: DNA
; ORGANISM: Aspergillus niger
US-10-662-914-29

Query Match 99.7%; Score 1345.4; DB 17; Length 2665;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1346; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 4 CTGGCAGTCCCGCTCGAGAAATCAATCCAGTTGCGATACGGTTCGATCAGGGGTATCAA 63
Db 842 CTGGCAGTCCCGCTCGAGAAATCAATCCAGTTGCGATACGGTTCGATCAGGGGTATCAA 901
Qy 64 TGCTTCTCCGAGCTTCGATCTTTGGGTCATACGCAACGGTTCCTCTCTCTGCGAAAC 123
Db 902 TGCTTCTCCGAGCTTCGATCTTTGGGTCATACGCAACGGTTCCTCTCTCTGCGAAAC 961
Qy 124 GAATCGGTCATCTCCCTGAGTGCCTCGCGGATGCGAGTCACTTTGCGTCAAGTCTC 183
Db 962 GAATCGGTCATCTCCCTGAGTGCCTCGCGGATGCGAGTCACTTTGCGTCAAGTCTC 1021
Qy 184 TCCCGTCAATGAGCGCGATATCCGACCGACTCCAAAGGCAAGAAATATCTCGCTCTCAT 243
Db 1022 TCCCGTCAATGAGCGCGATATCCGACCGACTCCAAAGGCAAGAAATATCTCGCTCTCAT 1081

Qy 244 GAGGAGATCCAGCAGACCGACCACTTTGACCGAAATATGCTTCTTGAAGACATAC 303
Db 1082 GAGGAGATCCAGCAGACCGACCACTTTGACCGAAATATGCTTCTTGAAGACATAC 1141
Qy 304 AACTACAGCTTTGGTTCAGATGACTGACTCCCTTCGGAGAAACAGGAGTAGTCAACTCC 363
Db 1142 AACTACAGCTTTGGTTCAGATGACTGACTCCCTTCGGAGAAACAGGAGTAGTCAACTCC 1201
Qy 364 GGCATCAAGTTCTTACAGCGGTACGAATCGTCTCAAGGAAACATCGTTCATTCGGA 423
Db 1202 GGCATCAAGTTCTTACAGCGGTACGAATCGTCTCAAGGAAACATCGTTCATTCGGA 1261
Qy 424 TCCTCTGGCTCCAGCGGTGATCGCTCCGGCAAGAAATTCATCGAGGGCTTCAGAGC 483
Db 1262 TCCTCTGGCTCCAGCGGTGATCGCTCCGGCAAGAAATTCATCGAGGGCTTCAGAGC 1321
Qy 484 ACCAAGCTGAAGGATCTCTGTCGCCAGCCCGCAATGCTCGCCAAAGATCGAGTGGTC 543
Db 1322 ACCAAGCTGAAGGATCTCTGTCGCCAGCCCGCAATGCTCGCCAAAGATCGAGTGGTC 1381
Qy 544 ATTTCCGAGGCGAGTCTATCCAAACAACACTCTCGACCCAGGACCTGCACTGTCTCGAA 603
Db 1382 ATTTCCGAGGCGAGTCTATCCAAACAACACTCTCGACCCAGGACCTGCACTGTCTCGAA 1441
Qy 604 GACACGGAATTTGGCGGATACCGTTCGAAGCCAAATTTCAACGCCACGTTGCTCCCTCAAT 663
Db 1442 GACACGGAATTTGGCGGATACCGTTCGAAGCCAAATTTCAACGCCACGTTGCTCCCTCAAT 1501
Qy 664 CGTCAAGCTTCGAGAACGAGCTGCTCGGTGTGACTCTCAGACACAGAGTGCACCTAC 723
Db 1502 CGTCAAGCTTCGAGAACGAGCTGCTCGGTGTGACTCTCAGACACAGAGTGCACCTAC 1561
Qy 724 CTCATGGACATGTGCTCTCTCGACACCATCTCCACGACCGCTCGACACCAAGCTGTCC 783
Db 1562 CTCATGGACATGTGCTCTCTCGACACCATCTCCACGACCGCTCGACACCAAGCTGTCC 1621
Qy 784 CCCTTCTGTGACCTGTTTCAACGATGACGAATGGATCAACTAGACTACCTCCAGTCTTG 843
Db 1622 CCCTTCTGTGACCTGTTTCAACGATGACGAATGGATCAACTAGACTACCTCCAGTCTTG 1681
Qy 844 AAAAAGTATTAGGCGCATGCTGAGTAAACCGCTCGGCCCGACCCAGGGCGTCCGGTAC 903
Db 1682 ACAAAGTATTAGGCGCATGCTGAGTAAACCGCTCGGCCCGACCCAGGGCGTCCGGTAC 1741
Qy 904 GCTAACGAGCTCATCGCCCGTCTGACCCACTCGCCCTGTCCAGATGACACAGTTCACAC 963
Db 1742 GCTAACGAGCTCATCGCCCGTCTGACCCACTCGCCCTGTCCAGATGACACAGTTCACAC 1801
Qy 964 CACACTTTGGACTCGAGCCCGCTACCTTTCCGCTCAACTCTACTCTCTACCGGACTTT 1023
Db 1802 CACACTTTGGACTCGAGCCCGCTACCTTTCCGCTCAACTCTACTCTCTACCGGACTTT 1861
Qy 1024 TCGCATGACAAACGGCATCATCTCCATTCTCTTTGTTTGGTTTGGTTTGGTTTGGTTTGG 1083
Db 1862 TCGCATGACAAACGGCATCATCTCCATTCTCTTTGTTTGGTTTGGTTTGGTTTGGTTTGG 1921
Qy 1084 CCGCTATCTACACAGCGTGGAGATATCACCCAGACAGATGATTCCTCGTCTGCTTGG 1143
Db 1922 CCGCTATCTACACAGCGTGGAGATATCACCCAGACAGATGATTCCTCGTCTGCTTGG 1981
Qy 1144 ACGGTTCCGTTTGGTTTGGTTTGGTTTGGTTTGGTTTGGTTTGGTTTGGTTTGGTTTGG 1203
Db 1982 ACGGTTCCGTTTGGTTTGGTTTGGTTTGGTTTGGTTTGGTTTGGTTTGGTTTGGTTTGG 2041
Qy 1204 CCGTGGTCCGTTTGGTTTGGTTTGGTTTGGTTTGGTTTGGTTTGGTTTGGTTTGGTTTGG 1263
Db 2042 CCGTGGTCCGTTTGGTTTGGTTTGGTTTGGTTTGGTTTGGTTTGGTTTGGTTTGGTTTGG 2101
Qy 1264 GCTTTGGGAGATGATACCCGGGATAGCTTTGTGAGGGGTTGAGCTTTGTAGATCTGGG 1323
Db 2102 GCTTTGGGAGATGATACCCGGGATAGCTTTGTGAGGGGTTGAGCTTTGTAGATCTGGG 2161
Qy 1324 GGTGATTGGCGGAGTGTGTTTGTCTTAG 1350

Db 2162 GGTGATTGGCGGAGTGTTTGCTTAG 2188

RESULT 14

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US-10-662-914-33
; Sequence 33, Application US/10662914
; Publication No. US20040126844A1
; GENERAL INFORMATION:
; APPLICANT: Lei, Xingren
; APPLICANT: Mullaney, Edward J
; APPLICANT: Ullah, Abul H.J.
; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTASES
; FILE REFERENCE: 19603/4261
; CURRENT APPLICATION NUMBER: US/10/662,914
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: 60/410,736
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 2665
; TYPE: DNA
; ORGANISM: Aspergillus niger
US-10-662-914-33

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Query Match          99.7%; Score 1345.4; DB 17; Length 2665;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1346; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY	4	CTGGCAGTCCCGCGCTCGAGAAATCAATCAAGTTGGATACGGTACATCAGGGGTATCAA	63
Db	842	CTGGCAGTCCCGCGCTCGAGAAATCAATCAAGTTGGATACGGTACATCAGGGGTATCAA	901
QY	64	TGCTTCTCCGAGACTTCGCATCTTTGGGGTCAATAGCAACGGTTCCTCTCTGGCAAC	123
Db	902	TGCTTCTCCGAGACTTCGCATCTTTGGGGTCAATAGCAACGGTTCCTCTCTGGCAAC	961
QY	124	GAATCGGTCACTCCCTGAGTGC CGCGCGGATGCAAGTACATTTGCTCAGTCTCTC	183
Db	962	GAATCGGTCACTCTCCCTGAGTGC CGCGCGGATGCAAGTACATTTGCTCAGTCTCTC	1021
QY	184	TCCCTCATGAGCGCGGTATPCGACGATCCAAGGGCAAGAAATATCTCCGCTCTCAT	243
Db	1022	TCCCTCATGAGCGCGGTATPCGACGATCCAAGGGCAAGAAATATCTCCGCTCTCAT	1081
QY	244	GAGGAGATCCAGCAGAACCGGACCACTTTGACGGAAATATGCTCTCTGGAAGACATAC	303
Db	1082	GAGGAGATCCAGCAGAACCGGACCACTTTGACGGAAATATGCTCTCTGGAAGACATAC	1141
QY	304	AATACAGCTTGGGTGCAGATGACTGCTCTTCGGAGAACAGGAGCTAGTCAACTCC	363
Db	1142	AATACAGCTTGGGTGCAGATGACTGCTCTTCGGAGAACAGGAGCTAGTCAACTCC	1201
QY	364	GGATCAAGTTCTACCAAGCGGTACGAATCGCTCACAAGGAACATCGTTCATTCAATCGA	423
Db	1202	GGATCAAGTTCTACCAAGCGGTACGAATCGCTCACAAGGAACATCGTTCATTCAATCGA	1261
QY	424	TCCTCTGCTCCAGCGCGGTGATCGCTCCGGCAAGAAATTCATCGAGGGCTTCAGAGC	483
Db	1262	TCCTCTGCTCCAGCGCGGTGATCGCTCCGGCAAGAAATTCATCGAGGGCTTCAGAGC	1321
QY	484	ACCAAGCTGAAGGATCTCTGTCGCCACGCCGGCCAAATCGTCGCCCAAGATCGACGTGTC	543
Db	1322	ACCAAGCTGAAGGATCTCTGTCGCCACGCCGGCCAAATCGTCGCCCAAGATCGACGTGTC	1381
QY	544	ATTTCCGAGGCCAGCTCATCCACAACACATCTCGACCCAGGACCTGCACTGTCTTCGAA	603
Db	1382	ATTTCCGAGGCCAGCTCATCCACAACACATCTCGACCCAGGACCTGCACTGTCTTCGAA	1441
QY	604	GACAGCGAATTTGGCCGATACCGTCAAGCAATTTCCGCCCAAGTTCGTCCCTCCATT	663
Db	1442	GACAGCGAATTTGGCCGATACCGTCAAGCAATTTCCGCCCAAGTTCGTCCCTCCATT	1501

Query Match 99.5%; Score 1343.8; DB 17; Length 2665;

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RESULT 15
US-10-662-914-15
; Sequence 15, Application US/10662914
; Publication NO. US20040126844A1
; GENERAL INFORMATION:
; APPLICANT: Lei, Xingen
; APPLICANT: Mullaney, Edward J
; APPLICANT: Ullsh, Abdul H.J.
; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTASES
; FILE REFERENCE: 19603/4261
; CURRENT APPLICATION NUMBER: US/10/662,914
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: 60/410,736
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 2665
; TYPE: DNA
; ORGANISM: Aspergillus niger
US-10-662-914-15

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Best Local Similarity 99.9%; Pred. No. 0; Matches 1345; Conservative 0; Mismatches 2; Indels 0; Gaps 0;									
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Db	842	CTGCAGTCCCGCTCGAGAAATCAATCCAGTTGGATACGGTCGATACGGGGTATCAA	901						
Qy	64	TGCTCTCCGAGACTCGCATCTTTGGGTCAATACGACCGTTCTCTCTCTGGCAAC	123						
Db	902	TGCTCTCCGAGACTCGCATCTTTGGGTCAATACGACCGTTCTCTCTCTGGCAAC	961						
Qy	124	GAATCGGTCACTCCCTCGAGTCCCGCGGATGACAGAGTCACTTTCGTCCAGTCCCT	183						
Db	962	GAATCGGTCACTCCCTCGAGTCCCGCGGATGACAGAGTCACTTTCGTCCAGTCCCT	1021						
Qy	184	TCCGTCATGAGCGCGGTATCCGACCGACTCCAGGCGAAGAAATACTCGGCTCTCAT	243						
Db	1022	TCCGTCATGAGCGCGGTATCCGACCGACTCCCGGCGAAGAAATACTCGGCTCTCAT	1081						
Qy	244	GAGGATCCAGCAGAACCGACCACTTTGACGGAATAATGCTTCTCTGAAGACATAC	303						
Db	1082	GAGGATCCAGCAGAACCGACCACTTTGACGGAATAATGCTTCTCTGAAGACATAC	1141						
Qy	304	AACATACGTTGGTGCAGATGACTGATCTCCCTTCGAGAACAGGAGTAGTCACTCC	363						
Db	1142	AACATACGTTGGTGCAGATGACTGATCTCCCTTCGAGAACAGGAGTAGTCACTCC	1201						
Qy	364	GGCATCAAGTTCTACACCGGTGCAATCGCTCAAGGAACATCGTTTCCATTCATCCGA	423						
Db	1202	GGCATCAAGTTCTACACCGGTGCAATCGCTCAAGGAACATCGTTTCCATTCATCCGA	1261						
Qy	424	TCCTCTGCTCCAGCCGCTGATCGCTCCGGAAGAAATTCATCGAGGGGTTCCAGAGC	483						
Db	1262	TCCTCTGCTCCAGCCGCTGATCGCTCCGGAAGAAATTCATCGAGGGGTTCCAGAGC	1321						
Qy	484	ACCAAGCTGAAGATCTCTGTCGCCAGCCCGGCAATCGTCGCCCAAGATCGAGTGGTC	543						
Db	1322	ACCAAGCTGAAGATCTCTGTCGCCAGCCCGGCAATCGTCGCCCAAGATCGAGTGGTC	1381						
Qy	544	ATTTCCGAGGCGAGTCAATCAACAACTCTCAACCCAGGCACTGCACTGTCTTCGAA	603						
Db	1382	ATTTCCGAGGCGAGTCAATCAACAACTCTCAACCCAGGCACTGCACTGTCTTCGAA	1441						
Qy	604	GACAGCAATTTGGCGGATACCGTCGAGGCAATTTCAACCGCCAGTTCGTCCTCCATT	663						
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Qy	664	CGTCAACGCTGGAGAACGACCTGTCCGCTGTGACTCTCAAGACACAGAGTCACTAC	723						
Db	1502	CGTCAACGCTGGAGAACGACCTGTCCGCTGTGACTCTCAAGACACAGAGTCACTAC	1561						
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Qy	904	GCTACGAGCTCATCGCCGCTGACCCACTCGCTGTCACGATGACACCGAGTCCAAAC	963						
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Qy	1024	TCGATGACACGAGCATCATCTCCATCTCTTGTGCTTTAGGTCTGTACAACGGCACTAAG	1083						

Db	1862	TCGCATGACAAAGCGCATCATCTCCATCTCTTTGCTTTAGGTCTGTACAACGGCACTAAG	1921
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Db	1922	CCGCTATCTTACCACGACCGTGGAGAAATATCACCCAGACAGATGGATTCTCGTCTGCTTGG	1981
Qy	1144	ACGGTTCGGTTTCTCGCGTTTGTACCGTCGAGATGATGATGATGATGATGATGATGATGATGAT	1203
Db	1982	ACGGTTCGGTTTCTCGCGTTTGTACCGTCGAGATGATGATGATGATGATGATGATGATGATGAT	2041
Qy	1204	CCGCTGCTCCGTTCTTGTAAATGATCGGTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1263
Db	2042	CCGCTGCTCCGTTCTTGTAAATGATCGGTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2101
Qy	1264	GCTTTGGGAGATGTACCCGGGATAGCTTTGTGAGGGGTTGAGCTTTGCTAGATCTGGG	1323
Db	2102	GCTTTGGGAGATGTACCCGGGATAGCTTTGTGAGGGGTTGAGCTTTGCTAGATCTGGG	2161
Qy	1324	GGTATTGGGCGGAGTGTCTTCTTAG	1350
Db	2162	GGTATTGGGCGGAGTGTCTTCTTAG	2188

Search completed: November 24, 2004, 13:02:13
Job time : 755 secs

Db 19 TGCACATAGTGTCAAGCTCGGATACCACTGCAACAGCCGTTTCTCAGCTCTGGGSCAA 78
Qy 97 TAGCACCGTTCTTCTCTCTGGCAACGAATCGGTCACTCCCTCAGGTGCGCGCGGA 156
Db 79 TATTCCCGCTATTCTCTCTGAAGTCAAGTCTCCCATCTCTCCGATGTACCGTCTGGA 138
Qy 157 TGCAGATCACTTTCGTCTAGTCTCTCTCTCGGTCTGAGGCGGTATCGACCGACTCC 216
Db 139 TGCACTATTACTTTTGCCCAAGTCTCTCCGATGGAGCAAGGTATCCCAAGAAAG 198
Qy 217 AAGGCAAGAAATACCTCGCTCTCAATGAGGAGATCCAGCAGACGCGACCTTTGAC 276
Db 199 AAAACCGAGCTACGCAAACTCTTTGATCGGATCAAGGAAACCAAGCAAGTCTTATGAG 258
Qy 277 GGAATAATGCTTCTGTAAGACATCAACTACAGCTTGGGTGAGATGACCTGATCCC 336
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Qy 517 CAATCGTCGCCAAGATCGAGTGGTCAATTTCCGAGGCCAGCTCATCCAAACACTCTTC 576
Db 499 GATAGACCCCTATCGTCAACTTGATTTATCCCTGAAGGAGTCCGAGTAACAATACACT 558
Qy 577 GACCCAGCACCTGCTCTTTCGAGACAGCAATTTGGCCGATACCGTTCGAGCCAAAT 636
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Qy 637 TTACCCGCGACGTTGCTGCTCCCTCATTCGTCACAGCTTCGAGAACGACCTGTCCGGTGTG 696
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Qy 757 ACCAGCACGTCGACACCAAGCTGTCCCTCTCTGTGACCTGTTTCAACCATGACGAATGG 816
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Qy 817 ATCAACTACGATACCTCAGTCTCTTGAAGAAATTTACGGCAATGGTGCAGTAAACCCG 876
Db 799 GTTGACTATGACTACTACGATCTCTTGGGAAATATTTACAGATATGGGCCAGGACGCCG 858
Qy 877 CTCGGCCGACCCAGGCGTCCGCTACGTAACGAGCTCATCGCCGCTGTGACCCACTCG 936
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Qy 937 CCTGTCCACGA 947
Db 919 CCCGTCAATGA 929

RESULT 2
CO011644
LOCUS
DEFINITION
EST799979 Coccidioides posadasii spherule cDNA library, 0.4 to 2.3
kb Coccidioides posadasii cDNA clone CIEB041 5' end, mRNA sequence.
ACCESSION
CO011644
VERSION
CO011644.1 GI:48518533
KEYWORDS
EST.
Coccidioides posadasii
SOURCE
Coccidioides posadasii

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Coccidioides.
1 (bases 1 to 810)
Gardner, M.J. and Cole, G.T.
Analysis of gene expression in Coccidioides posadasii mycelia and
spherules via expressed sequence tags
Unpublished (2003)
Other ESTs: EST799978
Contact: Gardner MJ
The Institute for Genomic Research
712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208
Email: gardner@tigr.org
Seq primer: M13 Reverse.
Location/Qualifiers
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Coccidioides posadasii spherule cDNA library, 0.4 to 2.3
kb"

ORIGIN
Query Match 19.9%; Score 268.6; DB 7; Length 810;
Best Local Similarity 59.6%; Pred. No. 1.8e-62;
Matches 476; Conservative 0; Mismatches 314; Indels 9; Gaps 1;

Qy 524 CGCCAAAGATCGAGTGTGTCATTTCCGAGGCCAGCTCATCCAAACACATCTCGACCCAG 583
Db 1 CCCCTATCGTCAACTTGTGATTTATCCCTGAGGAGATCGAGTAACAATACACTTGACCACT 60
Qy 584 GCACCTGCACTGTCTTTCGAAGACAGCGAATTTGGCCGATACCGTCGAAGCCCAATTTACCG 643
Db 61 CTTTATGCGAAAACTTCGAACAGGATAATTCAGGAAAGAGAGAGAGAGAGAGAGAGAGAGAG 120
Qy 644 CCAGCTTCCTCCCTCCATTCGTCAGCTCGAGAGACGACCTGTCCGCTGTGACTCTCA 703
Db 121 ACCTATTTGCCCCCTCCAAATTTTGAGCGTGTGAAAATCTCATCTCCCTGGCGCCATATTA 180
Qy 704 CAGACACAGAAAGTACCTACCTCATGGACATGTCTCTCTCGACACCATCTCCACACGCA 763
Db 181 CGGTACAGATGTGATCTTACCTCATGGATATGTCTCTCCACACCGGTGATGTTGACGC 240
Qy 764 CGGTGACACCAAGTGTCCCTCTCTGACCTGTTCAACCCATGACGAGTAATGATCAACT 823
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Qy 824 AGCACTACTCTCCAGTCTTGAAAAAGTATTACGGCCATGTGTCAGGTAACCCGCTCGGCC 883
Db 301 ATGACTACTACCACTCTCTTGGGAAATATTACAGATATGGCCAGGACGCCGCTCGGTG 360
Qy 884 CGACCCAGGGGTGCGGTACGCTAACGAGCTCATCGCCCTGTGACCCACTCGGCTGCTCC 943
Db 361 CTGAGCAAGGATGGGATTCACCAACGAATCATAGGCCGCTCTCAAAACACCCCGCTCA 420
Qy 944 AGGATGACACAGTTTCCAAACACACTTTTGGACTCGAGCCCGGCTACCTTTCCGCTCAACT 1003
Db 421 ATGACTCGACTTCCACCAACCGGACTCTTACTCTCACCCCGACCACTTCCCGCTAAAG 480
Qy 1004 CTACTCTCTACCGGACTTTTCGATGACCAAGGATCATCTCCATCTCTTTGCTTTAG 1063
Db 481 CCACCTCTCTACGCACTTTCAGCCATGATAACACTATGATAACGATCTTTCACGCCCTTGG 540
Qy 1064 GTCTGTAACGCGCACTAAGCGGTATCTACACGCGGTGAGAAATATACCCAGACAG 1123


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Db      541  GGCTGTTCAATAGACAGGAACCACTCCCTTACCCGATCCGGACCCCGTAGAGTCGG 600
Qy      1124  ATGGATCTCGTCTGTTGACAGGTTCCGTTTGGCTTTCGCGTTTGTAGTGCAGATGATGC 1183
Db      601  ACGGATTTTCGCGTCTGAGACGCTCCCGTTTCGCGGTAGGCTTACGTTGAGAAGATGA 660
Qy      1184  AGTGT-----CAGCGGAGCAGGAGCGGCTGGTCCGCTGCTTGGTTAATGATCGCG 1234
Db      661  AGTGTGACTGTCGCCAAGAGGATACGAGTTTGTGAGAACTTGTAAATGATCGTG 720
Qy      1235  TTGTCGCGCTGATAGGTGTCGCGTTGATGCTTTGGGGAGATGATCCCGGATAGCTTTG 1294
Db      721  TTATCCGCTCCATGGGTGAAGCTGACTCAATTAGGCCGTCGAGGTTAATGATTTG 780
Qy      1295  TGAGGGGTTGAGCTTTCG 1313
Db      781  TTAAGGGGCTGAGCTATGC 799

RESULT 3
CO004996/c
LOCUS      880 bp      mRNA      linear      EST 09-JUN-2004
DEFINITION      EST793331 Coccidioides posadasii spherule cDNA library, 0.4 to 2.3
                  kb Coccidioides posadasii cDNA clone CIEAM59 3' end, mRNA sequence.
ACCESSION      CO004996
VERSION
KEYWORDS      CO004996.1 GI:48511885
SOURCE
ORGANISM      Coccidioides posadasii
                  Coccidioides posadasii
                  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
                  Onygenales; Mitosporic Onygenales; Coccidioides.
REFERENCE      1 (bases 1 to 880)
AUTHORS      Gardner M.J. and Cole G.T.
TITLE      Analysis of gene expression in Coccidioides posadasii mycelia and
                  spherules via expressed sequence tags
JOURNAL      Unpublished (2003)
COMMENT      Other ESTs: EST793332
                  Contact: Gardner MJ
                  The Institute for Genomic Research
                  9712 Medical Center Drive, Rockville, MD 20850, USA
                  Tel: 301 838 3519
                  Fax: 301 838 0208
                  Email: gardneretigr.org.

FEATURES
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Query Match      18.7%; Score 252.8; DB 7; Length 880;
Best Local Similarity 61.6%; Pred. No. 4e-58;
Matches 426; Conservative 0; Mismatches 257; Indels 9; Gaps 1;

Qy      668  AAGCTCTGGAGACGACCTGTCGGTGTGACTCTCAGACAGACAGAGTACCTCA 727
Db      879  AGCGTGTGAAGAACTCATCTCCCTGGCGCAATATTACGGTCAAGATGTACTCA 820
Qy      728  TGGACATGTCCTCTTCGACACCATCTCCACAGACCGTCGACACCAAGCTGCCCT 787
Db      819  TGGATATGCTCTCTTCCACACCGTGATGTGACGCCGACGAGCAACTATCTCCAT 760
Qy      788  TCTGTACCTGTTCA CCCATGACGAATGGATCAACTACGACTACCTCCAGTCTCTGAAAA 847

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Db      759  TCTGCAACTCTTACCCAGCGGAATGGGTGACTATGACTACTACCACTCTCTTGGGA 700
Qy      848  AGTATTACGGCCANGTGCAAGTAACCCGCTCGGCCGACCCAGCGCTCGGCTACGCTA 907
Db      699  AATATTACAGATATGGCGCAGCGACCGCTCGGTGCTGAGCAAGCATGGGATTCACCA 640
Qy      908  ACGAGCTCATCGCCGCTGACCCACTCGCTGTCTCCAGATGACACCAAGTTCACACCA 967
Db      639  ACGAACTCATAGCCCGCTCTCAAAACACCCCGCTCAATGACTCGACTTCCACCAACCGCA 580
Qy      968  CTTTGGACTCGAGCCCGCTACCTTTCCGCTCAACTCTTACTCTCTTACCGGACTTTTCGC 1027
Db      579  CTCATTACCTCTCACCCGACCACTTCCGCTAAACGCCACTCTCTTACGACACTTCAGCC 520
Qy      1028  ATGACAACGGGATCATCTCCATTCTCTTTGCTTTAGTCTGTACACGGCACTAGCCGC 1087
Db      519  ATGATAACACTATGATTAACGATCTTACGGGCTTTGGGCTGTTCATATGACGGAACCA 460
Qy      1088  TATCTACCAACGACCGTGGAGATATCACCCAGACAGATGGATTCTCGTCTGCTTGGACGG 1147
Db      459  TCCCTTTGACCGCATCCGACCCCGTAGAGTCGGACGGATTTCTCGCTGCTGGACGG 400
Qy      1148  TTCCTTTGCTTCGGTTTGTACGTCGAGATGATGCACTGT-----CAGGCGGAGC 1198
Db      399  TCCCTTTGCGGTAGGCTTACGTTGAGAAAGATGAGTGCAGTGTGTCGCCAAGGAAG 340
Qy      1199  AGGAGCGCTGTCGCTGCTCTTGGTTAATGATCGGTTGTCCCGTCGATCGGTGTCGG 1258
Db      339  ATGACAGTTTGTGAGAACTTGTAAATGATCGTGTTTATCCGCTCCATGGGTGTAACG 280
Qy      1259  TTGATGCTTTGGGAGATGTACCCGGGATAGCTTTGTAGGGGGTTGAGCTTTGCTAGAT 1318
Db      279  TGGACTCATTAGCCGCTGCGAGGTAAATGATTTTGTAAAGGGCTGAGCTATSCAGCGA 220
Qy      1319  CTGGGGTGATGGCGGAGTGTGTTGCTTAG 1350
Db      219  GCGGGGGAATGGGACAGATGCTTTATTAAAG 188

CD459861      868 bp      mRNA      linear      EST 14-JUN-2004
F909_07a12_A F909 AAFECORC Fusarium graminearum simple_substrate
Gibberella zeae cDNA clone F909_07a12, mRNA sequence.
CD459861
CD459861.2 GI:48689893
EST.
Gibberella zeae
Gibberella zeae
Gibberella zeae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
REFERENCE      1 (bases 1 to 868)
AUTHORS      Watson R.J., Heyes R., Couroux P., De Moors A., Harris L.J.,
                  Hattori J., Lacroix C., Masotti M., Ouellet T., Robert L.S.,
                  Singh J.A., Spratt D. and Tinker N.A.
                  A cDNA library prepared from Fusarium graminearum grown on a simple
                  substrate
JOURNAL      Unpublished (2003)
COMMENT      On Jun 3, 2003 this sequence version replaced gi:31374601.
                  Contact: Watson, Robert.J.
                  Eastern Cereal and Oilseed Research Centre
                  Agriculture and Agri-food Canada
                  Bldg. 20, Central Experimental Farm, Ottawa, Ontario, KIA 0C6,
                  CANADA
                  Tel: (613) 759-1655
                  Fax: (613) 759-1701
                  Email: watsonrj@agr.gc.ca.
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FEATURES
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 Db 257 TGTAACTGGGACTCATTAGGCGGTGCGAGGTTAATGATTTGTAAAGGGGCTGAGCTAT 198
 Qy 1312 GCTAGATCTGGGGGTGATTGGCGGAGTGTTTTCCTTAG 1350
 Db 197 GCAGGAGCGGGGGAATGTGGGACAGATGCTTTTATAAG 159

RESULT 6
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 DEFINITION HO12K16w HO Hordeum vulgare cDNA clone HO12K16 3-PRIME, mRNA
 sequence.
 ACCESSION CK569249
 VERSION CK569249.1 GI:40954823
 KEYWORDS EST.
 SOURCE Hordeum vulgare
 ORGANISM Hordeum vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Pooideae; Triticeae; Hordeum.
 1 (bases 1 to 700)
 Zierold,U. and Schweizer,P.
 Barley ESTs from pathogen-attacked leaf epidermis
 Unpublished (2003)
 CONTACT: Patrick Schweizer
 Transcriptome Analysis, Cytogenetics Department
 Institute of Plant Genetics and Crop Plant Research (IPK)
 Corrensstr. 3, D-06466 Gatersleben, Germany
 Tel: 0049 (0)39482-5660
 Fax: 0049 (0)39482-5595
 Email: schweiz@ipk-gatersleben.de
 Insert length: 700 Std Error: 0.00
 Plate: 12 row: K column: 16
 Seq primer: T7.

FEATURES
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 hordel and tritici, respectively. Due to a cloning
 artefact caused by the kit, in most cases the EcoRI site
 is NOT present, as well as the EcoRI adapter used for
 cloning. To excise the insert, restriction sites upstream
 EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also
 due to the cloning system used Blue/white selection for
 recombinants is not 100% reliable. Average insert size is
 1.2 kb"

ORIGIN
 Query March 13.9%; Score 188; DB 7; Length 700;
 Best Local Similarity 59.5%; Pred. No. 2.6e-40;
 Matches 339; Conservative 0; Mismatches 225; Indels 6; Gaps 1;
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 Db 632 TCTCTCCATTCTGCCATTTATTCACTGCTTCTGAATGGCAGCGCTACGACTACTATGAA 573
 Qy 839 CCTTGAAAAAGTATTACGGCCATGTGTGAGTAACCCGCTCGCGCCGACCCCGGGCTGG 898

Db 572 CGTTGGAAGTACTACGGCTATTTCATGGGGTAATCCCTGGGACCCACTCAGGGCGTGG 513
 Qy 899 GCTACGCTAACGAGCTCATCGCCGCTCTGACCCACTCGCCTTCCACGATGACACGATT 958
 Db 512 GTTTTACTAATGAGCTGATTGACGACTCCTCGGTCTCTCTGTCATCGATCACGAGCA 453
 Qy 959 CCAACACACACTTTTGGACTCGAGCCCGGCTACCTTTCCGCTC-----AACTCTACTCTCT 1012
 Db 452 CCAATAACACACTTGTATCATGACCAAAAGACATTTCTCTCGATAATCAAACTACTCTCT 393
 Qy 1013 AGCGGACTTTTTCGATGATGACCAAGGATCATCTTCATTTCTTTTGTAGTCTGTGATA 1072
 Db 392 ATGCCGATTTTAGCCACGACAAACGACCTCCTAGTATATATTTGGCTGCTGTGTGCTCTACA 333
 Qy 1073 ACGGCACTAAGCGCTATCTACACGACCGTGGAGAAATATACCCAGACAGATGATTCT 1132
 Db 332 AAGATTCTCCGCATCTCTCAAGACGACGCTCCAACTTTCAACGCGCTTACGACTATT 273
 Qy 1133 COTCTGTTGGACGGTTCCGTTTGTTCGCTTTTGTACGTGAGATGATGAGTGTCAAG 1192
 Db 272 CCACTAGCGCTACTGTACCGTTTGGTGGCGGTATCTATTTCGAAAAGTTGAAATGCCAAG 213
 Qy 1193 CGGAGCAGGACCGCTGCTCGGTGCTTGTGTTAATGATCGGTTGTCGGCTGCATGGT 1252
 Db 212 ATATAGGGGAAGATTTAATCAGATAATTTGAAATGATCGGGTCTTCCGCTCGAATCTT 153
 Qy 1253 GTCCGGTTGATGCTTTGGGAGATGTACCCGGATAGCTTTGTGAGGGGGTTGAGCTTTG 1312
 Db 152 GCGGGCGAGATGAACCTGGTAGTGTACGTAGATAAATTTGTGATAGCTCGAATTTG 93
 Qy 1313 CTAGATCTGGGGTGAATTTGGGCGGAGTGT 1342
 Db 92 CGCGACAGATGGAAGATGGTCTGAGTGT 63

RESULT 7
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 DEFINITION AU248054 HL (Lolium multiflorum) Lolium multiflorum cDNA clone
 HL003E01-5, mRNA sequence.
 ACCESSION AU248054
 VERSION AU248054.1 GI:46505323
 KEYWORDS EST.
 SOURCE Lolium multiflorum (Italian ryegrass)
 ORGANISM Lolium multiflorum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Pooideae; Poaeae; Lolium.
 1 (bases 1 to 603)
 Ikeda,S.
 Lolium multiflorum EST Project
 Unpublished (2004)
 CONTACT: Seishi Ikeda
 Japan Grassland Farming Forage Seed Association(JFSA)
 Forage Crop Research Institute(FCRI)
 Higashikada 388-5, Nishinasuno, Tochigi 329-2742, Japan
 Tel: 81-287-37-6755
 Fax: 81-287-37-6757
 Email: siked@jfsass.or.jp
 contact:Tadashi Takamizo (takamizo@affrc.go.jp)
 National Institute of Livestock and Grassland Science, Nishinasuno
 Resistance gene analog.

FEATURES
 Location/Qualifiers
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Query Match 12.3%; Score 165.6; DB 1; Length 603;
Best Local Similarity 59.8%; Pred. No. 3.6e-34;
Matches 298; Conservative 0; Mismatches 194; Indels 6; Gaps 1;
QY 779 TGTCCTCCCTCTGTGACCTGTCACCATGACGAATGATCACTACGACTACCTCCAGT 838
Db 106 TCTCTCCATTTGGCATAATTAATCACTGCTGAAAGCGCGCTAGATTACTACAAA 165
QY 839 CTTTGAAGAAAGTATTACGGCCATGTTGACAGTTAACCGCTGCGCCGACCCAGGGCGT 898
Db 166 CAGTTGGAAGTACTACGGCTATTTCATGCGGTATCCACTCGGACCACTCAGGGCGT 225
QY 899 GCTACGCTACGAGCTATCGCGCTGTGACCACTGCGCTGTCACGATGACACAGTT 958
Db 226 GTTTTACTAATGAGCTAATTGACAGCTACTCGCTCTCCGCTCATCGATGATACAGCA 285
QY 959 CCAACCACTTTGAGCTCGAGCCGCTACTCTTTCGGCT-----CAACTCTACTCTCT 1012
Db 286 CTAATAACACACTGACACACATCCAGGAGTTCTCTCGATAGCCAACTGCTCTT 345
QY 1013 ACGCGGACTTTTCGATGACAAACGGGATCATCTCTTCTTTAGTCTGTACA 1072
Db 346 ACGCGGACTTTAGCCAGACAAACGACCTCACTAGCATATTGGCTGCGAGTTGGTCTCTACA 405
QY 1073 ACGGCACTAGCCGCTATCTACACGACCGTGGAGATATACCCAGACAGATGATTTCT 1132
Db 406 AATTTCTCCGCCACTCTCAAGACGAGCTCCATTTTAAAGCGACGTACGACTATT 465
QY 1133 CGTCTGCTTGACCGTTCCGTTTCTGCGTTTGTACGTCGAGATGATCGATGTCAGG 1192
Db 466 CGACTAGCGTACTGACCGTTCCGTTCCGCTGCTATCTATTTCGAAAAATTGAAGTGCCAAG 525
QY 1193 CGGAGCAGGACCGCTGCTGCTGCTGTTGTTATGATCGGTTGTCGCCGCTCATGGT 1252
Db 526 ATGACGCGAAGATATGATGCGGATCTTGGAATGATCGGGTCTTCCACTTCAATCT 585
QY 1253 GTCCGGTTGATGCTTTGG 1270
Db 586 GTGCGGAGATGCAATTGG 603

RESULT 8
AQ324539/6 802 bp DNA linear GSS 08-JAN-1999
LOCUS mgxb0019C01r CUGI Rice Blast BAC Library Magnaporthe grisea genomic
DEFINITION clone mgxb0019C01r, genomic survey sequence.

ACCESSION AQ324539
VERSION AQ324539.1 GI:4116391
KEYWORDS GSS.
SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM Magnaporthe grisea
REFERENCE Yu,Y., Zhu,H., Boyd,C.A., Gaudette,B., Gayle,A., Kingsbury,R.,
Phillips,K., Sasinsowski,M, Wing,R.A. and Dean,R.A.
TITLE A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
Genome
JOURNAL Unpublished (1998)
COMMENT Contact: Dean RA
Clemson University Genomics Institute
100 Jordan Hall, Clemson University, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemson.edu
Seq primer: GGAAACAGCTATGACCATG
Class: BAC ends
High quality sequence stop: 408.
Location/Qualifiers
1..802
/organism="Magnaporthe grisea"
/mol_type="genomic DNA"

FEATURES
source

/strain="70-15"
/db_xref="taxon:148305"
/clone="mgxb0019C01r"
/tissue_type="Protoplasts"
/lab_host="E. coli DH10B"
/clone_lib="CUGI Rice Blast BAC Library"
/note="Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII;
Rice blast is one of the most devastating fungal diseases
of rice world wide. It is a filamentous ascomycete with
a haploid genome (n=7) of approximately 40 Mbp. Rice
blast is an important model fungal pathogen for studying
numerous aspects of the fungal-host interaction. In
order to facilitate genome wide analysis, a BAC library
containing 9216 clones with an average insert size of 130
kbp was constructed. This library represents greater
than 25X genome coverage. High density colony filters
are available upon request."

ORIGIN

Query Match 11.5%; Score 155; DB 8; Length 802;
Best Local Similarity 57.3%; Pred. No. 3.1e-31;
Matches 303; Conservative 0; Mismatches 220; Indels 6; Gaps 1;
QY 773 CCAAGCTGTCCTTCTGTGACCTGTCACCCATGACGAATGATCACTACGACTACC 832
Db 537 CCACCTGTCGACGTTCTGCACTGTTTACGCAACGAGACTGGGAGGCATATGACTATC 478
QY 833 TCCAGTCTCTGAAAAGTATTACGCGCATGTTGTCAGGTAAACCGCTCGGCCGACCCAGG 892
Db 477 TCCACACTGGGNAAGTGGTATGTTACGGCAATGCGAACCCCTGGGCTCCACGCAAG 418
QY 893 GCGTCGGTACGCTAACGAGCTCATGCGCCGTGTGACCCACTGCGCTGTCACGATGACA 952
Db 417 GGGTGGGCTTCTGCAACGAGCTCATCGCGAGGCTGCTCCAAAAGCCCGTTGAAGACACA 358
QY 953 CCAGTTCCAAACACACTTTGGACTCGAGCCGCTTACCTTTCCGCTCAACTCTACTCTCT 1012
Db 357 CAAATACCACTCGACGCTCGACGACCCATCGAGTTCCCACTAGACAAAAGCTGT 298
QY 1013 ACGCGGACTTTTCGATGACAAACGCAATCATCTCCATTTCTTTTGTAGTCTGTACA 1072
Db 297 ACGCGGACTTTAGCCATGATAACGATATGCTGGGCATCTACGCGCGCTGGGGAATTACA 238
QY 1073 ACGGCACTAAGCGCTATCTACACGCGGTGGAGAATATCACCCAGACAGA-----TG 1126
Db 237 ACGCACGCGCCCGCATTCGGTCCCAAAAAGAGAGAGAGCGCGCAGGCTCAGCG 178
QY 1127 GATTCTCGTCTCTTGGACGCTTCGGTTCGCTTTCGCTTGTGTCGCTTGTGATGATGTCAGT 1186
Db 177 GGTTCGTCCAGCTGGCGGTACCGTTCCGACGCGAGGATGTTTGTGAAAAAATGACTT 118
QY 1187 GTCAGCGGAGCAGAGCGCGCTGGTTCGCTGCTGTTAATGATCGCTGTTGTCGCGTGC 1246
Db 117 GCGCAGGCGAGAACGAGGAGCTTGTGAGAACTCTGTCACGACGAGGTTGACGCGCTGC 58
QY 1247 ATGGGTGTCGCTGTCATGTTTGGGGAGATGTACCCGGGATAGCTTTGT 1295
Db 57 AGAACTGCGATCCGACACAGTATGGGTCGTGTCACGCTGAGCAAGTTCGT 9

RESULT 9

CD031252 620 bp mRNA linear EST 07-MAY-2003
LOCUS mgm005xE03f.b Mated culture Magnaporthe grisea cDNA clone
DEFINITION mgm005xE03 5', mRNA sequence.
ACCESSION CD031252
VERSION CD031252.1 GI:30413088
KEYWORDS EST.
SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthae.
1 (bases 1 to 620)
REFERENCE

AUTHORS Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,
Bhatterai,K. and Dean,R.A.
TITLE Expressed sequence tags from the rice blast fungus, Magnaporthe
grisea
JOURNAL Unpublished (2002)
COMMENT Contact: Ebbole DJ
Department of Plant Pathology & Microbiology
Texas A&M University
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
Tel: 979 845 4831
Fax: 979 845 6483
Email: d-ebbole@tamu.edu
Chromatogram file of this sequence is available, see contact
person: Best nr hit (April, 22, 2003) gb|AA52508.1| phytase
[Phielavia heterothallica] 239 3e-62
PCR Primers
FORWARD: T3 primer
BACKWARD: T7 primer
Plate: mgmt005 row: E column: 03
Seq primer: T3.
FEATURES
source Location/Qualifiers
1..620
/organism="Magnaporthe grisea"
/mol_type="mRNA"
/strain="4091-5-8 X 4136-4-3"
/db_xref="taxon:148305"
/clone="mgmt005x203"
/sex="Mat1-2 and Mat1-1 mixed culture"
/cell_type="mixed sexual development"
/dev_stage="asci, ascospores, perithecia, mycelium"
/clone_lib="Mated culture"
/notes="Vector: pBluescriptSK; Site 1: EcoRI; Site 2: XhoI;
Two mating types were co-cultivated over a filter paper on
oatmeal agar medium. After three days at 25 C plates were
transferred to 21 C. Perithecia with asci and ascospores
formed at the beginning of the third week. Material was
collected by scraping tissue from the filter paper.
Sequences were processed by one of two methods. Where a
full-length alignment to the M. grisea genome sequence was
available, the EST sequence was trimmed according to the
alignment, otherwise sequence quality was assessed using
phred/rpmap version 991019 and trimmed according to phd
files (0.05) and for vector seqs."

Query Match 11.2%; Score 150.8; DB 6; Length 620;
Best Local Similarity 55.1%; Pred. No. 4.3e-30;
Matches 343; Conservative 0; Mismatches 267; Indels 12; Gaps 2;
QY 567 CAACACTCTCGACCCAGGCACTGCACTGCTTCGGAAGACAGCGAATGGCCGATACCGT 626
DB 1 CAACACGCTAAACCATACCTATGTACTGCTTTGAGAACACCAACTCGCAAGGAAGC 60
QY 627 CGAAGCCAAATTCACCGCCACGTTGCTCCCTCCATTGCTCAACGTCCTGGAGAACGACCT 686
DB 61 CCAAAGAGTTTATGAGAGTGCCATGGCGGCATACAGACGCTTGAAACAGCGCT 120
QY 687 GTCGGTGTGACTCTCACAGACACAGAGTAGTACCTACCTCATGGACATGTGCTCTCGA 746
DB 121 GGAGGGTGCAAACTCAGCAACCAAGCAAGCGGTGCAGATCATGGAGCTCTGCCCGTTGA 180
QY 747 CACCACTCTCACAGACACCGTCCACACCAAGCTGCCCCCTTCTGTGACTGTTACCCA 806
DB 181 GACCGTGGCAGATCCCAAG-----CCACCTGTGGCAGTCTGCACGCTGTTACGCA 234
QY 807 TGACGAATGGATCAACTACGACTACCTCCAGTCTCTTGAAAGATATATAGGCCATGGTGC 866
DB 235 ACGAGACTGGAGGCATATGACTATCTCCAGACACTGGGGAGTGTATGTTACGCCAA 294
QY 867 AGTAAACCGCTCGGCCGACCCAGGCGGTGCGCTACGCTAACGAGCTCATCGCCCGTCT 926
DB 295 TGGCAACCCCTTGGGCTCCACGCAAGGGTGGGCTTCGTCAACGAGCTCATCGCGAGGT 354

QY 927 GACCCACTCGCTTCACGATGACACGAGTTCCAAACACACTTTTGGACTCGAGCCCGC 986
DB 355 GCTCCAAAAGCCGTTGAAGACCAACAAATACCACTCGAGCGTCGACAGGACCCATC 414
QY 987 TACCTTTCCGCTCAACTCTCTCTAGCGGACATTTTTCGATGACAAAGCGATCATCTC 1045
DB 415 GACGTTCCCATCTAGACAAAAGCTGTAGCCGACATTTAGCCATGATAGATATCTGGG 474
QY 1047 CATCTCTTTGCTTTAGGTCTGTACACGGCACTTAAGCCGCTATCTACACGACGTGGA 1106
DB 475 CATCTACGCGCGCTGGGGATTTACACGCCACGCCCCCGATTCCGTCCTCCCAAAAAGGA 534
QY 1107 GAATATCCCCAGACAGA-----TGGATTCTCGTCTCTTGGACGGTTCGGTTGCTTC 1160
DB 535 GAGAAAGGAGCGCGCAGGAGCTCAGCGGGTTCTCGGCCAGCTGGGGGGTACCGGTGCGAGC 594
QY 1161 GCGTTTGTACGTCGAGATCATG 1182
DB 595 GAGGATGTTTGGTGA AAAAGG 616
RESULT 10
CF882569/c
LOCUS
DEFINITION
tric030xn08.g1 T.reesei mycelial culture, Version 6 October 2003
Hypocrea jecorina cDNA clone tric030xn08, mRNA sequence.
ACCESSION
CF882569
VERSION
CF882569.1 GI:38137251
KEYWORDS
EST.
SOURCE
Hypocrea jecorina (anamorph: Trichoderma reesei)
ORGANISM
Hypocrea jecorina
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
REFERENCE
1 (bases 1 to 544)
Diener,S.E., Dunn-Coleman,N., Foreman,P., Houfek,T.D.,
Teunissen,P.J.M., van Solingen,P., Dankmeyer,L., Mitchell,T.K.,
Ward,M. and Dean,R.A.
TITLE
Characterization of the protein processing and secretion pathways
in a comprehensive set of expressed sequence tags from Trichoderma
reesei
JOURNAL
FEMS Microbiol. Lett. 230 (2), 275-282 (2004)
COMMENT
Contact: Ralph A. Dean
Fungal Genomics Laboratory
North Carolina State University
Campus Box 7251, Raleigh, NC 27695, USA
Tel: 919-513-0020
Fax: 919-513-0024
Email: ralph_dean@ncsu.edu
Seq primer: LT-R1 primer.
FEATURES
source Location/Qualifiers
1..544
/organism="Hypocrea jecorina"
/mol_type="mRNA"
/strain="QM6a"
/db_xref="taxon:51453"
/clone="tric030xn08"
/dev_stage="mycelia"
/clone_lib="T.reesei mycelial culture, Version 6 October
2003"
/note="Vector: PREP3V; Site 1: Not I/Sal I; Mycelial
culture grown from 24 hrs to 6 days with varying carbon
and Nitrogen sources and concentrations."

Query Match 10.3%; Score 138.4; DB 7; Length 544;
Best Local Similarity 57.7%; Pred. No. 1.1e-26;
Matches 247; Conservative 0; Mismatches 181; Indels 0; Gaps 0;
QY 914 TCATGCCCGCTGACCCACTCGCTGTCCAGATGACACAGTTCCAAACACACTTTGG 973
DB 544 TGATTGCCAGGCTCAGCGCGAGCGCTGTGCACTGGACGACGACGACGACGACGCTCG 485
QY 974 ACTCGAGCGCGGCTACCTTTTCGGCTCAACTCTCTCTACGCGGACTTTTCGATGACA 1033

[illegible]

RESULT 11				
AJ274007	AJ274007	581 bp	linear	EST 29-DEC-1999
LOCUS				
DEFINITION	AJ274007 Metarhizium anisopliae ARSEF 2575 Metarhizium anisopliae			
	CDNA clone Ma#1628, mRNA sequence.			

ORIGIN	CONSTRUCTED IN THE UNIDIRECTIONAL SAMBOA VECTOR, CHIRAPY			
Query Match	8.7%	Score 117.6;	DB 1;	Length 581;
Best Local Similarity	55.0%	Pred. No. 5.7e-21;		
Matches	275.	Conservative	0:	Mismatches 219; Indels 6: Gaps 2;

QY	122	ACGAATCGGTCA	TCTCCCTGAGGTGCCCGCGGATGCAGAGTCACTTTGCGTCAGGTC	181
Db	194	ACAAGGGATCT	ATTAAAGCTGACATCCCGTCGGGATCGAGGTCACTTTGCTTCAATCT	253
QY	182	TCTCCCGTCA	TGAGCGCGGTATCCGACCGACTCCAAGGGCAAGAAATATCCGGTCTCA	241
Db	254	TGTCGACAT	GGGTCCGCCAACCGACGCGCGCAAGTCCAAAGGCTTCAAGGACCTGG	313
QY	242	TTGAGGAGAT	TCAGCAGAACGGCACCATTTTGACGGAAAAATATGCTTCCCTGAACACAT	301
Db	314	TTGAGCGGAT	TCCAAAAGACGTTCAAGGACATATGGGAAGGGCTTCGAGTTTCTCAAAAGATT	373
QY	302	ACAAC	TACAGCTTGGGTGCAGATGACCTGACTCCCTTCGGAAGAACAGGAGCTAGTCAACT	361
Db	374	ACAAGTAT	ACTCTAGGTTCTGACGACCTCACCCCTTGGCGAGCAGGAAATGGTCAAGT	433
QY	362	CGGCA	TCAAAGTTTCTACAGCGGTACGAATCGTCAAGGAA--CATCGTTCCAATTC	418
Db	434	CTGGA	AAAAAAGTTTCTTCAAGCGCTATCAGAAGTTACGGAGGATTCGATCCCATCCCTTTG	493
QY	419	TCGGAT	CTCTGGCTCCAGCCGGGTGATCGCTCCGGCAAGAAATTCATCGAGGGGCTTCC	478
Db	494	TTGAG	CCCTCGGGCTCTGAAGAGTCGTATGTCTACGCGCAAGATTTTGTTCATGGCTTCT	553
QY	479	AGAGCA	CCAAGCTGAAGGAT	498
Db	554	ACAAG	CCCAAGGGCAAGAAT	573

RESULT 12	CN808226	1059 bp	linear	EST 27-MAY-2004
LOCUS	BloodEST0309	Metarhizium anisopliae	ARSEF	2575 from insect blood
DEFINITION	Metarhizium anisopliae	CDNA clone B688.5',	mRNA sequence.	

ORIGIN

Query Match	8.7%;	Score 117.6;	DB 7;	Length 1059;
Best Local Similarity	55.0%;	Pred. NO. 6.5e-21;		
Matches	275;	Conservative	0;	Mismatches 219; Indels 6;
Gap	2;			

355 TTCTGGGCTTTGGCTTTCGGCGGAGATCGATCAGACTCCAAAGTCATCGTTTAAACAAGCGCT 414
Db
62 AATGCTTCTCCGAGACTTCGATCTTTGGGTCATATACGACCGCTTCTTCTCTCTCGCAA 121
QY
415 CTGACCCACAGATTTTCGACGACTGGGGCCAGTACTCGCGTACTTCTC---AGCAC 471
Db
122 ACGAATCGGTCATCTCCCTCGAGTGCCCGCCGGATGAGAGTCACTTCGCTCAGGTCC 181
QY
472 ACAAGGATCTATTAAAGCTTGACATCCCGTCCGGATCGGAGTCACTTTGCTTCAATCT 531
Db
182 TCTCCGTCATGAGCGGCTATCCGACGACTCCAGGCGCAAGAAATATCTCGCTCTCA 241
QY
532 TGCTCGACATGGTCCCGCAACCCGACGCGCGGAAAGTCCAAAGGCTTACAGGACTGG 591
Db
242 TTGAGGATCCAGCAGCAAGCGACCACTTTGACGGAATAATGCTTCTCTGAAACAT 301
QY
592 TTGAGCGATCCAAAPAGAGCTCAAGGACTATGGAAGGCTCTGAGTTTCTCAAAGATT 651
Db
302 ACAACTACAGTTGGGTGAGATGACCTGACCTCCCTTCGAGAACAGGAGTACTCACT 361
QY
652 ACAAGTACTCTAGGTTCTGACGACCTCAACCCCTTTGGCGGAGCAAGAAATGCTCAAGT 711
Db
362 CCGCATCAAGTTCTACAGCGGTACGAATCGCTCAACAAGGAA---CATCGTTCCCATCA 418
QY
712 CTGGAATAAGATTTCTCAAGGCTATCAGAAGTTAGCGGAGGATTCGACCCATCCCTTTG 771
Db
419 TCGATCTCTGCTCAGCGCGCTGATCGCTCCGCAAGAAATTCATCGAGGCTTCC 478
QY
772 TTCGAGCTCGGCTCTGAAGAGTCTGATGTCAGCGCAAGATTTGTTTCATGGCTTCT 831
Db
479 AGACCAACAGCTCAAGGAT 498
QY
832 ACAAGCGAAGGCAAGAAAT 851
Db

RESULT 13
CD030240/c
LOCUS
DEFINITION mgmt001x016.f b Mated culture Magnaporthe grisea cDNA clone EST 07-MAY-2003
ACCESSION CD030240
VERSION CD030240.1 GI:30412076
KEYWORDS EST.
SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.

1 (bases 1 to 586)
Ebbel,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,
Bhatnagar,K. and Dean,R.A.
Expressed sequence tags from the rice blast fungus, Magnaporthe
grisea
Unpublished (2002)
Contact: Ebbel DJ
Department of Plant Pathology & Microbiology
Texas A&M University
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
Tel: 979 845 4831
Fax: 979 845 6483
Email: d-ebbel@tamu.edu
Chromatogram file of this sequence is available, see contact
person; Best nr hit (April. 22, 2003) gb|AA52508.1| phytase
[Thielavia heterothallica] 166 5e-44
PCR Primers
FORWARD: T3 primer
BACKWARD: T7 primer
Plate: mgmt001 row: 0 column: 16
Seq primer: T3.

FEATURES
source
1..586
/organism="Magnaporthe grisea"
/mol_type="mRNA"
/strain="4091-5-8 X 4136-4-3"

/db_xref="taxon:148305"
/clones="mgmt001x016"
/sex="Mat1-2 and Mat1-1 mixed culture"
/cell_type="mixed sexual development"
/dev_stage="asci, ascospores, perithecia, mycelium"
/clone_lib="Mated culture"
/note="Vector: pBluescriptSK; Site 1: EcoRI; Site 2: XhoI;
Two mating types were co-cultivated over a filter paper on
oatmeal agar medium. After three days at 25 C plates were
transferred to 21 C. Perithecia with asci and ascospores
formed at the beginning of the third week. Material was
collected by scraping tissue from the filter paper.
Sequences were processed by one of two methods. Where a
full-length alignment to the M. grisea genome sequence was
available, the EST sequence was trimmed according to the
alignment, otherwise sequence quality was assessed using
phredphrap version 991019 and trimmed according to phd
files (0.05) and for vector seqs."

ORIGIN

Query Match 8.6%; Score 115.6; DB 6; Length 586;
Best Local Similarity 55.6%; Pred. No. 2e-20; Indels 8; Gaps 2;
Matches 266; Conservative 0; Mismatches 204;
QY 874 CCGCTCGGCCCCACCCAGGGCGTCCGCTACGCTAACGAGCTCATGCCCGTCTGACCAC 933
Db 586 CCCCTGGGCTCCACGCAAGGGTGGGTTCACGAGCTCATGCCAAGTTGCTCAA 527
QY 934 TCGCTGTCCAGATGACACCGAGTTCCACACACTTTGGACTCGAGCCGGCTACCTTT 993
Db 526 AGGC--GTTGAAGGCCACACAATAACCAACTCGACGCTCGACGACCCATCGAGTTC 469
QY 994 CGCTCAACTCTACTCTTACCGGAGCTTTTCGCTATGACGAGCTCATGCCGATCATCTCCATTCTC 1053
Db 468 CCACTAGACAAAAGCTGTACCGGCTTTAGCCATGATACGATATGCTGGCATCTAC 409
QY 1054 TTGCTTTAGTCTGTACAAACGCACTAAGCCGCTATCTACACACCGTGTGAGAAATATC 1113
Db 408 GCGCGCTGGGATTTACAAACGCAACGCGCCCGCTCGTCCCAAAAAGAAAGAG 349
QY 1114 ACC-----CAGACAGATGCTTCTGCTGCTTGGACGGTTCCGTTTCTTCGGGTTTG 1167
Db 348 AGCGCGCAAGCTCAGCGGGTTCGCTCCAGCTGGCGGTACCGTTCCGACGAGGATG 289
QY 1168 TAGCTCGAGATGATGCAAGTGTGAGCGGAGCAGGAGCGCTGGTCCGTCGTTGTTTAAT 1227
Db 288 TTGTTGAAAAAATGACTTCCGAGGGCAGAACGAGGAGCTTGTGAGAAATCCTGGTCAAC 229
QY 1228 GATCGGTTGTCCTCCGCTGATGGTTCGCTGATGCTTTGCGGAGATGTACCCGGAT 1287
Db 228 GACAGGGTGACCGCGCTGCAGAACTCGATGCCAGATGGGTCTGTCAGCTGAGC 169
QY 1288 AGCTTTGTGAGGGGGTTGAGCTTTGCTAGATCTGGGGGTGATTTGGCGGAGTGTTTTG 1345
Db 168 AGTTCTTGAGAGCTTAAGCTTTGCGAGGATGGAGGTTCGCTGGGATCAATGTTTG 111

RESULT 14
CD646039 520 bp mRNA linear EST 12-JUL-2004
LOCUS CD646039
DEFINITION SSPG841 SS pectin Sclerotinia sclerotiorum cDNA similar to Phytase,
mRNA sequence.
ACCESSION CD646039
VERSION CD646039.1 GI:40545822
KEYWORDS EST.
SOURCE Sclerotinia sclerotiorum
ORGANISM Sclerotinia sclerotiorum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
Helotiales; Sclerotiniaceae; Sclerotinia.
1 (bases 1 to 520)
Li,R., Rimmer,R., Buchwaldt,L., Sharpe,A., Seguin-Swartz,G.,
Coutu,C. and Hegedus,D.
Interaction of Sclerotinia sclerotiorum with a Resistant Brassica
TITLE

napus Cultivar: Expressed Sequence Tag Analysis Identifies Genes
Associated with Fungal Pathogenesis
Fungal Genet. Biol. 41 (8), 735-753 (2004)
Contact: Hegedus D.
Agriculture & Agri-Food Canada
107 Science Place, Saskatoon, Canada, S7N 0X2
Email: hegedusd@agr.gc.ca
Insert Length: 520 Std Error: 0.00.
Location/Qualifiers
Source
1. .520

FEATURES

/organism="Sclerotinia sclerotiorum"
/mol_type="mRNA"
/strain="100"
/db_xref="taxon:5180"
/tissue_type="mycelia"
/lab_host="E. coli"
/clone_lib="SS pectin"
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; Sclerotinia sclerotiorum (strain 100) was
inoculated into minimal salts citrus pectin medium and
allowed to grow for 10 days at room temperature prior to
harvest. Single pass sequencing was done using the T3
(ATTACCTCACTAAAGGA) and T7 primers
(TAATACGACTCACTATAGG)."

ORIGIN

Query Match 8.5%; Score 114.2; DB 6; Length 520;
-Best Local Similarity 59.9%; Pred. No. 4.8e-20;
Matches 191; Conservative 0; Mismatches 128; Indels 0; Gaps 0;
QY 1030 GACACCGCATCATCTCCATCTCTTTCTTAGTCTGTACACGGCAGCTAACCGCTA 1089
DB 2 GACAATGACATGACTGCTATATCTCCGCTCTTGGTGTATTAATCTCCACAGCGCATTA 61
QY 1090 TCTACCGACCGTGGAGATATCACCCAGACAGATGATTCCTGCTGTGACCGTT 1149
DB 62 TCAAAACGAGAGAGATGCGTGTGCAACGAGTGGCTATTACGCGAGTTGTCGGTA 121
QY 1150 CGTTTGTCTCGGTTTGTAGTGTGAGATGATGATGATGATGATGATGATGATGATG 1209
DB 122 CCATTTCAGCGAGGATGTATGTGAGAGATGACCTGTGCGGTGAGATGAGAGTTG 181
QY 1210 GTCCGTGCTTGGTTAATGATCGGTTGTCCGCTGCAATGGGTGTCCGTTGATGCTTTG 1269
DB 182 GTTAGAGTTATTTGTTAATGACCGGCTGTACAANTAAAGACATGTGTTGTTGATGAATG 241
QY 1270 GGGAGATGTACCCGGATAGCTTTGTGAGGGGTTGAGCTTTGCTAGATCTGGGGGTGAT 1329
DB 242 GCGAGATGTGATGTCAAGTTTGTAGAGATTTGAGCTTTGCTAGTGAAGGGGTGAC 301
QY 1330 TGGGGGAGTGTGTTTGTCTT 1348
DB 302 TGGGGAGCTGCTTTACTT 320

RESULT 15
LOCUS AQ255459 837 bp DNA linear GSS 23-OCT-1998
DEFINITION mgxb0014M15r CUGI Rice Blast Library Magnaporthe grisea genomic
clone mgxb0014M15r, genomic survey sequence.
ACCESSION AQ255459
VERSION AQ255459.1 GI:3779774
KEYWORDS GSS.
SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM Magnaporthe grisea
REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.
1 (bases 1 to 837)
AUTHORS Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.
TITLE A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
Genome
JOURNAL Unpublished (1998)

COMMENT

Contact: Dean RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson University, Clemson, SC 29634
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Fax: 864 656 4293
Email: rdean@clemson.edu
Seq primer: GGAACAGCTATGACCATG
Class: PAC ends
High quality sequence start: 60
High quality sequence stop: 277.

FEATURES

Location/Qualifiers
Source
1. .837
/organism="Magnaporthe grisea"
/mol_type="genomic DNA"
/strain="70-15"
/db_xref="taxon:148305"
/clone="mgxb0014M15r"
/tissue_type="Protoplasts"
/lab_host="E. coli DH10B"
/clone_lib="CUGI Rice Blast BAC Library"
/note="Vector: pBRACWICH; Site 1: HindIII; Site 2: HindIII;
Rice blast is one of the most devastating fungal diseases
of rice world wide. It is a filamentous ascomycete with
a haploid genome (n=7) of approximately 40 Mbp. Rice
blast is an important model fungal pathogen for studying
numerous aspects of the fungal-host interaction. In
order to facilitate genome wide analysis, a BAC library
containing 9216 clones with an average insert size of 130
kbp was constructed. This library represents greater
than 25X genome coverage. High density colony filters
are available upon request."

ORIGIN

Query Match 8.0%; Score 107.6; DB 8; Length 837;
Best Local Similarity 53.6%; Pred. No. 3.5e-18;
Matches 224; Conservative 0; Mismatches 194; Indels 0; Gaps 0;
QY 662 TTCTGCTCAAGCTCGGAGAACGACCTGTCCGGTGTGACTCTCACACACACAGAGTGACCT 721
DB 119 TTATACAGCATAGCTGGGATTTTCAGGTGCTGGGTAAACCGGTCAAGACGTTGTAA 178
QY 722 ACCTCATGACATGTGCTCTTTCGACACCATCTCCACCAGCACCGTCGACACCAAGCTGT 781
DB 179 ATCTTATGGGACTGTGCACCATGGAACCGTAATCTTTGGGCCCAACTTGGCAACTTT 238
QY 782 CCCCTTCTGTGACCTGTTCACCATGACGATGATCACTACGACTACCTCCAGTCTCT 841
DB 239 CACCGCTTTCGATCTGTTTACGGAAGCAGATTTGGTTAAATATATGTTTACTTGTCCAGG 298
QY 842 TGAAAAAGTATTACGGCCATGTCAGGTAAACCCGCTCGGCCCGACCCAGGGCGTCCGCT 901
DB 299 TGCAAAAATGTTACAGATACGGAACCGTAATCTTTGGGCCCAACTATGCGGTGGGAT 358
QY 902 ACGCTAACGAGCTCATCGCCGCTGACCCACTGCGCTGTCCAGATGACACCACTTCCA 961
DB 359 GGGTAACGAACTTATTGACGATTAACCCGAAAGCCAGTCCAAAGATCAAAACCATGTCCA 418
QY 962 ACCACACTTTGGACTTCGAGCCCGGTACTCTTCGGCTCAACTCTACTCTCTACCGGACT 1021
DB 419 ATACGACACTTTCGACATGAACCCGGAACTTACTCTTACAGGCAATTTGATGCTGATT 478
QY 1022 TTTCGATGACACCGGATCATCTCCATCTCTCTTTGCTTTAGGTCTGTACACGCGAC 1079
DB 479 TTATCCATACGAGACGATATTATAGGATTTACGCGCGGTTTGGGCTATTTAACGCCCC 536

Search completed: November 24, 2004, 11:09:45
Job time : 4738 secs